

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:09:50 ; Search time 31 Seconds
(without alignments)
756.018 Million cell updates/sec

Title: US-09-817-814-2
Perfect score: 1118
Sequence: 1 MAPAEVGFGLGLEGGQ.....PRPVDPERVPELYKDLIMYT 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	211	21	AAB18635 Amino acid sequenc
2	1118	100.0	211	22	AAU09931 Human fibroblast g
3	1118	100.0	211	22	AGG5666 Human fibroblast g
4	1118	100.0	211	22	AAU02081 Human fibroblast g
5	1118	100.0	211	22	AAU02081 Human fibroblast g
6	1074	96.1	212	22	AAU02080 Human fibroblast gro
7	778.5	69.6	220	18	AAW11548 Amino acid sequenc
8	774.5	69.3	208	13	AAW11548 Amino acid sequenc
9	774.5	69.3	208	13	AAW11548 Amino acid sequenc
10	774.5	69.3	208	15	AAW11548 Amino acid sequenc
11	774.5	69.3	208	16	AAW11548 Amino acid sequenc

12	774.5	69.3	208	16	AAW11547 FGF-9. Homo sapie
13	774.5	69.3	208	18	AAW11547 Amino acid sequenc
14	774.5	69.3	208	19	AAW11547 Fibroblast growth
15	774.5	69.3	208	19	AAW53024 Fibroblast growth
16	774.5	69.3	208	21	AAW10299 Fibroblast growth
17	774.5	69.3	208	21	AAW10299 Human FGF-9 protei
18	774.5	69.3	208	21	AAW10299 FGF-9, SEQ ID NO:1
19	774.5	69.3	208	21	AAW10299 Human fibroblast g
20	774.5	69.3	208	21	AAW10299 Human fibroblast g
21	774.5	69.3	208	22	AAW10299 Murine fibroblast
22	774.5	69.3	208	22	AAW10299 Human fibroblast g
23	774.5	69.3	208	22	AAW10299 FGF9 protein. Hom
24	774.5	69.3	208	22	AAW10299 Human fibroblast g
25	774.5	69.3	208	22	AAW10299 Human fibroblast g
26	774.5	69.3	208	22	AAW10299 Human fibroblast g
27	774.5	69.3	208	22	AAW10299 Human fibroblast g
28	769.5	68.8	207	15	AAW56504 Human fibroblast g
29	758.5	67.8	205	13	AAW27209 Glia activating fa
30	758.5	67.8	205	15	AAW56506 Glia activating fa
31	758.5	67.8	206	13	AAW27211 Glia activating fa
32	758.5	67.8	206	13	AAW27212 Glia activating fa
33	758.5	67.8	206	15	AAW56507 Glia activating fa
34	742	66.4	175	15	AAW56508 Glia activating fa
35	742	66.4	176	15	AAW56509 Glia activating fa
36	742	66.4	177	13	AAW27208 Glia activating fa
37	742	66.4	178	13	AAW27210 Glia activating fa
38	729	65.2	159	15	AAW56510 Glia activating fa
39	729	65.2	160	15	AAW56511 Glia activating fa
40	708.5	63.4	207	20	AAW05474 Human FGF-16 prote
41	708.5	63.4	207	21	AAW58429 Human fibroblast g
42	708.5	63.4	207	22	AAW56562 Human fibroblast g
43	708.5	63.4	207	22	AAW56562 Human fibroblast g
44	708.5	63.4	207	22	AAW56562 Human fibroblast g
45	705.5	63.1	207	20	AAW05473 Rat FGF-16 protein

ALIGNMENTS

RESULT 1	
AAB18635	
ID	AAB18635 standard; Protein; 211 AA.
XX	
AC	AAB18635;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	Amino acid sequence of human fibroblast growth factor (FGF)-20.
XX	
KW	PD10-VEGFuc; gene delivery vector; eye disease; neovascular disease;
KW	neurotrophic factor; anti-angiogenic factor; eye disease; glaucoma;
KW	macular degeneration; diabetic retinopathy; retinitis pigmentosa;
KW	inherited retinal degeneration; surgery-induced retinopathy;
KW	retinal detachment; photic retinopathy; toxic retinopathy;
KW	trauma-induced retinopathy; wet age related macular degeneration;
KW	ARMD; retinopathy; fibroblast growth factor-20; FGF-20.
OS	Homo sapiens.
XX	
PN	WO2000054813-A2.
XX	
PD	21-SEP-2000.
XX	
PF	15-MAR-2000; 2000WO-US07062.
XX	
PR	15-MAR-1999; 99US-0124460.
PR	06-JAN-2000; 2000US-0174984.
XX	
PA	(CHIR) CHIRON CORP.
PA	(REGC) UNIV CALIFORNIA.
XX	
PI	Manning WC, Dwarki VJ, Rendahl K, Zhou S, McGee LH, Lau D;
PI	Flannery JG, Miller S, Wang F, Di Polo A;

XX WPI: 2000-618862/59.
DR N-PSDB; AAA75630.
XX
PT Treating or preventing eye diseases or inhibiting neovascular disease
PT of the eye, comprises intraocularly administering a gene delivery
PT vector that directs expression of neurotrophic factors or
PT anti-angiogenic factors -
XX
PS Disclosure: Fig 29; 86pp; English.
XX
CC The present sequence represents human fibroblast growth factor (FGF)-20.
CC FGF-20 is expressed using a gene delivery vector of the invention.
CC Vectors of the invention are used for treating or preventing eye
CC diseases, or inhibiting neovascular disease of the eye. The gene
CC delivery vector directs the expression of one or more neurotrophic
CC factors, or anti-angiogenic factors, such that the disease of the eye
CC is prevented or treated. The gene delivery vectors are useful for
CC treating or preventing diseases of the eye such as macular degeneration,
CC diabetic retinopathy, inherited retinal degeneration such as retinitis
CC pigmentosa, glaucoma, surgery-induced retinopathy, retinal detachment,
CC photic retinopathy, toxic retinopathy or trauma-induced retinopathy and
CC for inhibiting neovascular diseases such as wet age related macular
CC degeneration (ARM) or retinopathy of prematurity.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 1118; DB 21; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQQVGSFLLPAGERPPLLGERRSAERSARGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQQVGSFLLPAGERPPLLGERRSAERSARGPGAAQLAHL 60
QY 61 HGILRRQLYCRTFHQLQILPDGSGVQGTQDHSFLGILEFISVAVGLVIRGVDGLYL 120
DB 61 HGILRRQLYCRTFHQLQILPDGSGVQGTQDHSFLGILEFISVAVGLVIRGVDGLYL 120
QY 121 MNDKGLYGSEKLTSECIFRQGFENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
DB 121 MNDKGLYGSEKLTSECIFRQGFENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
QY 181 SKRHQKTFHLPVPDPERVPELYKDLLMYT 211
DB 181 SKRHQKTFHLPVPDPERVPELYKDLLMYT 211
RESULT 2
ID AAU09931 standard; Protein; 211 AA.
XX AAU09931;
XX
XX 15-JAN-2002 (first entry)
XX Human fibroblast growth factor-like (FGF-L) polypeptide sequence.
XX Human; fibroblast growth factor-like; FGF-L; agonist; antagonist;
KW vulnerable; virucide; hepatotropic; antiinflammatory; gut disorder;
KW hepatitis; diabetes; wound healing; ulcer; liver disorder;
KW lung disorder; angiogenesis.
XX
XX Homo sapiens.
XX
XX WO200168854-A2.
XX
XX 20-SEP-2001.
XX
XX 13-MAR-2001; 2001WO-US08013.
XX
XX 13-MAR-2000; 2000US-188786P.
XX
XX

PA (AMGE-) AMGEN INC.
XX
XX PI Jing S, Bass MB;
XX
DR WPI: 2001-596910/67.
DR N-PSDB; AAS15701.
XX
XX New fibroblast growth factor-like polypeptide and polynucleotide for
PT diagnosis, prevention and treatment of diseases, disorders or
PT conditions involving the central nervous system, teeth, heart, liver or
PT adipose tissue -
XX
XX Claim 3; Fig 1; 116pp; English.
XX
XX The present invention relates to new isolated fibroblast growth
XX factor-like (FGF-L) nucleic acid molecules and polypeptides. The FGF-L
XX polypeptide is useful for determining whether a compound inhibits FGF-L
XX polypeptide, and also for identifying a compound that binds to the
XX polypeptide. The FGF-L polypeptides of the invention are useful for
XX treating, preventing or ameliorating a medical condition or an FGF-L
XX polypeptide-related disease, condition or disorder such as wound healing
XX disorders, ulcers, gut disorders, lung disorders, liver disorders as
XX hepatitis and diabetes. The invention is also useful for diagnosing a
XX pathological condition or susceptibility to a pathological condition in
XX a subject and is useful for modulating levels of FGF-L in an animal.
XX other uses are detecting or quantifying the amount of FGF-L polypeptide
XX and for identifying or developing novel agonists and antagonists of the
XX FGF-L polypeptide signalling pathway which are useful for treating one
XX or more diseases or disorders, and also as an immunogen for producing
XX antibodies for in vivo imaging. The present sequence encodes the human
XX FGF-L polypeptide of the invention. The present sequence represents the
XX human FGF-L polypeptide of the invention.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 1118; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQQVGSFLLPAGERPPLLGERRSAERSARGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQQVGSFLLPAGERPPLLGERRSAERSARGPGAAQLAHL 60
QY 61 HGILRRQLYCRTFHQLQILPDGSGVQGTQDHSFLGILEFISVAVGLVIRGVDGLYL 120
DB 61 HGILRRQLYCRTFHQLQILPDGSGVQGTQDHSFLGILEFISVAVGLVIRGVDGLYL 120
QY 121 MNDKGLYGSEKLTSECIFRQGFENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
DB 121 MNDKGLYGSEKLTSECIFRQGFENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
QY 181 SKRHQKTFHLPVPDPERVPELYKDLLMYT 211
DB 181 SKRHQKTFHLPVPDPERVPELYKDLLMYT 211
RESULT 3
ID AAG65666 standard; protein; 211 AA.
XX AAG65666;
XX
XX 07-JAN-2002 (first entry)
XX Human fibroblast growth factor (FGF)-20.
XX
XX Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic;
KW fat deposition; vulnery; antiulcer; dermatological; anorectic;
KW antidiabetic; antiinflammatory; cytostatic; hepatic; virucide;
KW neuroprotectant; pulmonary; gene therapy; vaccine; human.
XX
XX Homo sapiens.
XX

PN WO200172957-A2.
XX 04-OCT-2001.
XX 02-APR-2001; 2001WO-IB00664.
XX 31-MAR-2000; 2000US-0540118.
XX (ITOH/) ITOH N.
XX Itoh N;
XX WPI; 2001-611623/70.
XX New human nucleic acid encoding fibroblast growth factor-like peptide,
PT useful for treatment and diagnosis of e.g. wounds and inflammatory
PT bowel disease -
XX
XX Disclosure; Fig 3; 172pp; English.
XX
CC The invention provides human nucleic acids encoding fibroblast growth
CC factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by
CC standard recombinant methodology and are mitogenic for a wide range of
CC cells, inducing differentiation and proliferation, and inhibiting
CC deposition of fat. The FGF-like polypeptides, polynucleotides and
CC specific antibodies and modulators are useful for treating a very wide
CC range of diseases and conditions, e.g. wounds, ulcers, skin aging,
CC obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral
CC hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of
CC the eye, etc., also for maintaining organs before transplant and
CC supporting culture of primary cells and tissues. Sequences AAG5647-67
CC represent amino acid sequences of some members of the FGF family.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 1118; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQGVSHFLLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQGVSHFLLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
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DB 61 HGILRRQLYCRTHFLQILPDGVSQGTQDHSFLFGILEFISVAVGLVSRGVDGSLYL 120
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DB 121 MNDKGLYSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
QY 181 SKRHQKFTFLPRPDPVPERVPELYKDLLMYT 211
DB 181 SKRHQKFTFLPRPDPVPERVPELYKDLLMYT 211

RESULT 4
AAU02081
ID AAU02081 standard; Protein; 211 AA.
XX
AC AAU02081;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human fibroblast growth factor 20, FGF-20.
XX
KW Human: fibroblast growth factor 20; FGF-20; Parkinson's disease;
KW substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen;
KW antibody; neuro-degenerative disease; tendonitis; wound healing;

KW stroke; ischaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 170..186
FT /label= Heparin_binding_site
XX
PN WO200131008-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29237.
XX
XX 22-OCT-1999; 99US-0161162.
PR 08-MAR-2000; 2000US-0187856.
XX
XX (CHIR) CHIRON CORP.
XX (KYOU) UNIV KYOTO.
XX
XX Itoh N, Kavanaugh WM;
XX WPI; 2001-308642/32.
DR N-PSDB; AAS03277.
XX
XX New human and rat Fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions -
XX
XX Claim 12; Fig 8; 73pp; English.
XX
CC The sequence is Human fibroblast growth factor 20, FGF-20. The FGF
CC polypeptides and nucleic acids encoding them are useful for providing
CC trophic support for cells in a patient, especially a patient with
CC Parkinson's disease, and FGF-20 is additionally used to treat patients
CC with conditions of the substantia nigra. The polypeptides and nucleic
CC acids are useful for alleviating human brain conditions by slowing
CC degeneration, restoring function of, or increasing the number of,
CC dopaminergic neurons. The polypeptides and nucleic acids are also
CC useful for alleviating cochlea-associated disease by slowing of the
CC degeneration of or restoring or maintaining normal function of the
CC structure of cochlea, where the disease is otosclerosis, Cogan's
CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
CC hearing loss, congenital malformations, autoimmune disease-related
CC hearing loss, age-related hearing loss, deafness associated with lack
CC of FGF receptor and ischaemia-related hearing disturbance. Other
CC diseases thought to be amenable to FGF therapeutic activity include
CC neuro-degenerative diseases, tendonitis, wound healing, stroke and
CC ischaemia. The polypeptides can be used to screen for agonists and
CC antagonists. Epitope bearing fragments of the FGF-20 polypeptides can be
CC used to raise anti-FGF-20 antibodies.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 1118; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQGVSHFLLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQGVSHFLLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
QY 61 HGILRRQLYCRTHFLQILPDGVSQGTQDHSFLFGILEFISVAVGLVSRGVDGSLYL 120
DB 61 HGILRRQLYCRTHFLQILPDGVSQGTQDHSFLFGILEFISVAVGLVSRGVDGSLYL 120
QY 121 MNDKGLYSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
DB 121 MNDKGLYSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
QY 181 SKRHQKFTFLPRPDPVPERVPELYKDLLMYT 211
DB 181 SKRHQKFTFLPRPDPVPERVPELYKDLLMYT 211

RESULT 5
AAB62817
ID AAB62817 standard; Protein; 211 AA.
XX
AC AAB62817;
XX
DT 02-MAY-2001 (first entry)
XX
DE Human fibroblast growth factor-CX (FGF-CX) amino acid sequence.
XX
KW Fibroblast growth factor-CX; FGF-CX; wound healing; haematopoiesis;
KW cell growth; proliferation; tumour; restenosis; psoriasis; human;
KW Dupuytren's contracture; Kaposi sarcoma; rheumatoid arthritis;
KW cartilage repair; bone repair; exostosis; hallux valgus deformity;
KW achondroplasia; cerebral lesion; cerebral oedema; senile dementia;
KW Alzheimer's disease; diabetic neuropathy; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200107595-A2.
XX
PD 01-FEB-2001.
XX
PF 27-JUL-2000; 2000WO-US20405.
XX
PR 27-JUL-1999; 99US-0145899.
PR 31-JAN-2000; 2000US-0494585.
PR 03-JUL-2000; 2000US-0609543.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Jeffers M, Shimkets RA, Prayaga SK, Boldog FL, Yang M, Burgess C;
PI Fernandes E, Herrmann JL, Larochele WJ, Lichenstein H;
XX
XX WPI; 2001-159717/16.
DR N-PSDB; AAF62049.
XX
XX New human fibroblast growth factor FGF-CX polypeptide, useful for
PT treating tissue proliferation disorders such as tumors, restenosis,
PT psoriasis, diabetic complications, Kaposi sarcoma and rheumatoid
PT arthritis -
XX
PS Claim 1; Fig 1; 128pp; English.
XX
CC This invention relates to human fibroblast growth factor-CX (FGF-CX) and
CC the DNA sequence encoding it. FGF-CX protein and polynucleotide sequences
CC are useful for treating or preventing a disorder associated with aberrant
CC expression, processing or physiological interactions of FGF-CX
CC characterised by insufficient or ineffective growth of a cell or tissue.
CC FGF-CX is also useful for promoting growth of cells which are in the
CC vicinity of a wound, vascular system, those involved in haematopoiesis or
CC erythropoiesis, cells in the lining of the gastrointestinal tract or
CC cells in hair follicles. Other uses include, inhibiting cell growth.
CC FGF-CX is useful for treating, preventing or delaying a tissue
CC proliferative disorder such as tumours, restenosis, psoriasis,
CC Dupuytren's contracture, diabetic complications, Kaposi sarcoma, and
CC rheumatoid arthritis. Compositions containing FGF-CX can be used to
CC stimulate cartilage or bone repair. Compositions containing FGF-CX
CC binding agents can be used to treat diseases such as multiple or solitary
CC hereditary exostosis, hallux valgus deformity and achondroplasia. FGF-CX
CC may be used in diagnosing or treating glial cell related disorders,
CC cerebral lesions or to treat cerebral oedema, senile dementia,
CC Alzheimer's disease, or diabetic neuropathy. FGF-CX also has
CC osteogenesis-promoting activity and can be used for treating bone
CC fractures and osteoporosis. FGF-CX polypeptides may be used as platelet
CC increasing agents, or for treating cerebral nervous diseases. The present
CC sequence represents the human FGF-CX protein.
XX
SQ Sequence 211 AA;

Query Match 100.0%; Score 1118; DB 22; Length 211;

Best Local Similarity 100.0%; Pred. No. 2.9e-111;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGEGQGVGSHFLPPAGERPPLLGERRSAAERSARGGPGCAOIAHL 60
DB 1 MAPLAEVGGFLGGLGEGQGVGSHFLPPAGERPPLLGERRSAAERSARGGPGCAOIAHL 60
QY 61 HGILRRRLQYCRGTGFLHQLIPDGSVQGTRODHSIFGLIEFISVAVGLSVIRGVDGLYL 120
DB 61 HGILRRRLQYCRGTGFLHQLIPDGSVQGTRODHSIFGLIEFISVAVGLSVIRGVDGLYL 120
QY 121 MNDKGYLGSEKLTSECIFREQEENWYNTSSNIYKHGDTGRYFVALNKDGTPRDGR 180
DB 121 MNDKGYLGSEKLTSECIFREQEENWYNTSSNIYKHGDTGRYFVALNKDGTPRDGR 180
QY 181 SKRHQKTHFLPRVDPERPVELYKDLMLMT 211
DB 181 SKRHQKTHFLPRVDPERPVELYKDLMLMT 211
RESULT 6
AAU02080
ID AAU02080 standard; Protein; 212 AA.
XX
AC AAU02080;
XX
DT 07-SEP-2001 (first entry)
XX
DE Rat fibroblast growth factor 20, FGF-20.
XX
KW Rat; fibroblast growth factor 20; FGF-20; Parkinson's disease;
KW substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen;
KW antibody; neuro-degenerative disease; tendonitis; wound healing;
KW stroke; ischaemia.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Peptide 56..70
FT /label= Epitope
FT /note= "Peptide used to raise anti-FGF-20 antibodies"
FT Binding-site 170..186
FT /label= Heparin_binding_site
FT Peptide 176..189
FT /label= Epitope
FT /note= "Peptide used to raise anti-FGF-20 antibodies"
XX
PN WO200131008-A2.
XX
XX 03-MAY-2001.
XX
PD 20-OCT-2000; 2000WO-US29237.
XX
PF 22-OCT-1999; 99US-0161162.
PR 08-MAR-2000; 2000US-0187856.
XX
XX (CHIR) CHIRON CORP.
XX (KYOU) UNIV KYOTO.
XX
XX Itoh N, Kavanaugh WM;
XX
XX WPI; 2001-308642/32.
DR N-PSDB; AAS03276.
XX
XX New human and rat Fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions -
XX
PS Claim 45; Fig 7; 73pp; English.

XX The sequence is Rat fibroblast growth factor 20, FGF-20. The FGF
 CC polypeptides and nucleic acids encoding them are useful for providing
 CC trophic support for cells in a patient, especially a patient with
 CC Parkinson's disease, and FGF-20 is additionally used to treat patients
 CC with conditions of the substantia nigra. The polypeptides and nucleic
 CC acids are useful for alleviating human brain conditions by slowing
 CC degeneration, restoring function of, or increasing the number of,
 CC dopaminergic neurons. The polypeptides and nucleic acids are also
 CC useful for alleviating cochlea-associated disease by slowing
 CC degeneration of or restoring or maintaining normal function of the
 CC structure of cochlea, where the disease is otosclerosis, Cogan's
 CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
 CC hearing loss, congenital malformations, autoimmune disease-related
 CC of FGF receptor and ischaemia-related hearing disturbance. Other
 CC diseases thought to be amenable to FGF therapeutic activity include
 CC neuro-degenerative diseases, tendonitis, wound healing, stroke and
 CC ischaemia. The polypeptides can be used to screen for agonists and
 CC antagonists. Epitope bearing fragments of the FGF-20 polypeptides can be
 CC used to raise anti-FGF-20 antibodies.

XX
 SQ Sequence 212 AA;

Query Match 96.1%; Score 1074; DB 22; Length 212;
 Best Local Similarity 95.3%; Pred. No. 1.5e-106;
 Matches 201; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAPLAEVGGFLGLEGIGQVQSGHFLPPAGERPPLLGERRSAERSARGGPGCAQLAHL 60
 DB 1 MAPTEVGAFLGLEGIGQVQSGHFLPPAGERPPLLGERRGALRGPGSVELAHL 60
 QY 61 HGILRRQLYCRGFGHLQILPDGSGVQGTQDHSFLGILEFISVAVGLVSIRGDSGLYIG 120
 DB 61 HGILRRQLYCRGFGHLQILPDGSGVQGTQDHSFLGILEFISVAVGLVSIRGDSGLYIG 120
 QY 121 MNDKGLYSGSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
 DB 121 MNGKGLYSGSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGA 180
 QY 181 SKRHQKTFHFLPRVDPERPVELYKDLLMYT 211
 DB 181 SKRHQKTFHFLPRVDPERPVELYKDLLVYT 211

RESULT 7
 AAW11548
 ID AAW11548 standard; Protein; 220 AA.

XX AAW11548;

XX 17-SEP-1997 (first entry)

XX Amino acid sequence of chicken FGF9 encoded by FGF9:pET-3C.

XX Mouse; chicken; fibroblast growth factor 9; FGF9; detection;
 KW fibroblast growth factor receptor 3; FGF9; cartilage repair;
 KW bone repair; antagonist; anti-FGF9 antibody; endochondromas;
 KW solitary hereditary exostosis; multiple hereditary exostosis;
 KW hallux valgus deformity; achondroplasia; synovial chondromatosis.
 XX Gallus domesticus.

XX Key Location/Qualifiers

XX Misc-difference 216

XX /note= "Given in the specification as J, encoded by TGA"

XX WO9641523-A1.

XX 27-DEC-1996.

XX 12-JUN-1996; 96WO-IL00011.

XX

PR 12-JUN-1995; 95US-0000137.
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX Yayan A;
 XX WPI: 1997-065215/06.
 DR N-PSDB; AAT58531.
 XX Medical and diagnostic use of fibroblast growth factor 9 - and
 PT recombinant fibroblast growth factor 9 DNA
 PS Claim 13; Fig 2; 32pp; English.

XX The sequences given in RAW1547-48 represent mouse and chicken
 CC fibroblast growth factor 9 (FGF9) respectively. FGF9 may be used in the
 CC method of the invention for detecting fibroblast growth factor receptor 3
 CC (FGFR3) in a sample or tissue. The method comprises contacting the
 CC sample or tissue with FGF9, allowing formation of receptor-ligand pairs,
 CC and detecting any FGFR3-FGF9 pairs. Compositions containing FGF9 can
 CC be used to increase FGFR3 activity, esp. to stimulate cartilage or bone
 CC repair. Compositions containing FGF9 antagonists or FGF9 binding agents
 CC (e.g. anti-FGF9 antibodies) can be used to treat diseases caused by an
 CC excess of FGF9 or overactivity of FGFR3, esp. multiple or solitary
 CC hereditary exostosis, hallux valgus deformity, achondroplasia, synovial
 CC chondromatosis and endochondromas.

XX Sequence 220 AA;

Query Match 69.6%; Score 778.5; DB 18; Length 220;
 Best Local Similarity 71.6%; Pred. No. 5.8e-75;
 Matches 151; Conservative 19; Mismatches 32; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFLGLEGIGQVQSGHFLPPAGERPPLLGERRSAERSARG---GPGAAQL 57
 DB 8 MAPLGEVGNVFGQDAV--PFGNVNPA--ADSPVLLSDHLGQAE--AGGLPRGAVTDL 61
 QY 58 AHLHGLIRRLQLYCRGFGHLQILPDGSGVQGTQDHSFLGILEFISVAVGLVSIRGDSGL 117
 DB 62 DHLKGLIRRLQLYCRGFGHLEIFPNGTIQGTQDHSRFRGILEFISVAVGLVSIRGDSGL 121
 QY 118 YLGMNDKGLYSGSEKLTSCIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRD 177
 DB 122 YLGMNKGELYSGSEKLTQECVREQFEENWNTYSSNLKHKVDTGRRYFVALNKDGTPRE 181
 QY 178 GAKSRHQKTFHFLPRVDPERPVELYKDLL 208
 DB 182 GTRTKRHQKTFHFSRPRVDPKVPVELYKDLL 212

RESULT 8

AAR27207
 ID AAR27207 standard; Protein; 208 AA.

XX AAR27207;

XX 20-MAY-1998 (first entry)

XX Glia activating factor #1.

XX GAF; stimulates glial cell growth; cerebral nerve cell lesions;
 KW cerebral oedema; alzheimers disease; senile dementia;
 KW diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
 KW stimulates megakaryocytes; increase platelets; haematopoietic cells;
 KW immunocompetent cells; vascular smooth muscle cells; bone fractures;
 KW osteogenesis promoting activity; osteoporosis; cerebral tumours;
 KW stimulates cultured cells.

XX Homo sapiens.

XX EP503297-A.

XX 16-SEP-1992.

PD

```

XX PF 13-FEB-1992; 92EP-0102385.
XX OS Homo sapiens.
XX PN EP503297-A.
XX PD 16-SEP-1992.
XX XX 13-FEB-1992; 92EP-0102385.
XX PF 14-FEB-1991; 91JP-0020860.
XX PR 04-SEP-1991; 91JP-0224454.
XX PR 10-JAN-1992; 92JP-0003399.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX XX Kondo T, Kurokawa T, Naruo K, Seko C;
XX PI WPI; 1992-309482/38.
XX DR WPI; 1992-309482/38.
XX XX Glia activating factor and its DNA - specifically promotes growth
XX PT of glial cells, for treating e.g. cerebral lesions, Alzheimer's
XX PT disease, diabetic neuropathies, etc., also in diagnosis
XX PS Claim 1; Pg5; 7pp; English.
XX CC This sequence represents a glia activating factor. It stimulates the
XX CC growth of glia cells and can be used to accelerate healing of cerebral
XX CC lesions or treat cerebral oedema, alzheimers disease, senile dementia,
XX CC or diabetic neuropathy. It also stimulates fibroblasts (to increase the
XX CC healing of burns, wounds, ulcers, etc) megakaryocytes (to increase the
XX CC no. of platelets), haematopoietic, immunocompetent and vascular smooth
XX CC muscle cells. It is also expected to have osteogenesis-promoting activity
XX CC (for treating bone fractures and osteoporosis) Assay of this factor may
XX CC be useful in diagnosis of cerebral tumours, and antibodies against could
XX CC be used to treat such tumours. It can also be used as a reagent for
XX CC stimulating growth of cultured cells. Dosage is lng-0.1mg/kg/day.
XX SQ Sequence 208 AA;

Query Match 69.3%; Score 774.5; DB 13; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.5e-74;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFGLGEGQQVGSFLLPPAGERPPLIGERRSAAERSARG---GPGAAOL 57
DB 1 MAPLGEVNGYGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPVATDL 54
QY 58 AHLHGILRRRLCYCRTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
DB 55 DHLKGILRRRLCYCRTGFHLEIFPFGTIQGTRODHSRFGILEFISVAVGLVSRGVDSGL 114
QY 118 YLGMNDKGLYGSSEKLTSECFRQFENWNTYSSNLYKHVDGTGRYFVALNKDGTPRD 177
DB 115 YLGMNEKGLYGSSEKLTQECVFRQFENWNTYSSNLYKHVDGTGRYFVALNKDGTPRE 174
QY 178 GARSKRHKQKTHFLPRPVDPERVPPELYKDIL 208
DB 175 GTRTKRHKQKTHFLPRPVDPKVPPELYKDIL 205

RESULT 10
AAR56505
ID AAR56505 standard; peptide; 208 AA.
XX AC AAR56505;
XX XX 06-MAR-1995 (first entry)
XX DE Glia activating factor (GAF) peptide.
XX KW Glia activating factor; GAF; testing; detection; antibody; cancer;
XX KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.
XX KW stimulates cultured cells.

XX PF 13-FEB-1992; 92EP-0102385.
XX OS Homo sapiens.
XX PN EP503297-A.
XX PD 16-SEP-1992.
XX XX 13-FEB-1992; 92EP-0102385.
XX PF 14-FEB-1991; 91JP-0020860.
XX PR 04-SEP-1991; 91JP-0224454.
XX PR 10-JAN-1992; 92JP-0003399.
XX PA (TAKE ) TAKEDA CHEM IND LTD.
XX XX Kondo T, Kurokawa T, Naruo K, Seko C;
XX PI WPI; 1992-309482/38.
XX DR WPI; 1992-309482/38.
XX XX Glia activating factor and its DNA - specifically promotes growth
XX PT of glial cells, for treating e.g. cerebral lesions, Alzheimer's
XX PT disease, diabetic neuropathies, etc., also in diagnosis
XX PS Claim 1; Fig 19; 87pp; English.
XX CC This sequence represents a glia activating factor. It is expressed
XX CC in monkey COS-7 cells. It stimulates the growth of glia cells and
XX CC can be used to accelerate healing of cerebral lesions or treat cerebral
XX CC oedema, alzheimers disease, senile dementia, or diabetic neuropathy. It
XX CC also stimulates fibroblasts (for accelerating healing of burns, wounds,
XX CC ulcers, etc) megakaryocytes (to increase the no. of platelets),
XX CC haematopoietic, immunocompetent and vascular smooth muscle cells. It is
XX CC also expected to have osteogenesis-promoting activity (for treating
XX CC bone fractures and osteoporosis) Assay of this factor may be useful in
XX CC diagnosis of cerebral tumours, and antibodies against could be used to
XX CC treat such tumours. It can also be used as a reagent for stimulating
XX CC growth of cultured cells. Dosage is lng-0.1mg/kg/day.
XX SQ Sequence 208 AA;

Query Match 69.3%; Score 774.5; DB 13; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.5e-74;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFGLGEGQQVGSFLLPPAGERPPLIGERRSAAERSARG---GPGAAOL 57
DB 1 MAPLGEVNGYGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPVATDL 54
QY 58 AHLHGILRRRLCYCRTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
DB 55 DHLKGILRRRLCYCRTGFHLEIFPFGTIQGTRODHSRFGILEFISVAVGLVSRGVDSGL 114
QY 118 YLGMNDKGLYGSSEKLTSECFRQFENWNTYSSNLYKHVDGTGRYFVALNKDGTPRD 177
DB 115 YLGMNEKGLYGSSEKLTQECVFRQFENWNTYSSNLYKHVDGTGRYFVALNKDGTPRE 174
QY 178 GARSKRHKQKTHFLPRPVDPERVPPELYKDIL 208
DB 175 GTRTKRHKQKTHFLPRPVDPKVPPELYKDIL 205

RESULT 9
AAR27213
ID AAR27213 standard; Protein; 208 AA.
XX AC AAR27213;
XX XX 20-MAY-1998 (first entry)
XX DE Glia activating factor #7.
XX KW GAF; stimulates glial cell growth; cerebral nerve cell lesions;
XX KW cerebral oedema; alzheimers disease; senile dementia;
XX KW diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
XX KW stimulates megakaryocytes; increase platelets; haematopoietic cells;
XX KW immunocompetent cells; vascular smooth muscle cells; bone fractures;
XX KW osteogenesis promoting activity; osteoporosis; cerebral tumours;
XX KW stimulates cultured cells.

```


KW FGF-9; fibroblast growth factor; cytotoxic conjugate; fusion protein;
 KW saporin; cytostatic; tumor; diabetes; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 68 /note- "Cys may be replaced by Ser"
 FT
 XX
 PN W09503831-A.
 XX
 PD 09-FEB-1995.
 XX
 XX 27-JUL-1994; 94WO-US08511.
 XX
 PF 02-AUG-1993; 93US-0099924.
 XX
 PR 29-OCT-1993; 93US-0145829.
 XX
 XX (PRIZ-) PRIZM PHARM INC.
 PA (WHIT-) WHITTIER INST DIABETES & ENDOCRINOLOGY.
 XX
 PI Baird AJ, Lappi DA, Sosnowski BA;
 XX
 DR WPI; 1995-082038/11.
 XX
 XX New monogenous preparations of cytotoxic conjugates and DNA -
 PT contain fibroblast growth factors and cytotoxic agents for
 PT treating FGF conditions such as tumours, diabetes and rheumatoid
 PT arthritis.
 XX
 PS Disclosure; Page 115-116; 128pp; English.
 XX
 CC Novel fusion proteins comprise FGF linked to saporin. FGF-1 to -9
 CC may be used, pref. mutants in which at least 1 Cys residue is
 CC replaced by conservative Ser substitutions. The fusion proteins
 CC are potent cytotoxic agents to cells bearing the FGF receptor.
 XX
 XX Sequence 208 AA;
 SQ

Query Match 69.3%; Score 774.5; DB 16; Length 208;
 Best Local Similarity 70.6%; Pred. No. 1.5e-74;
 Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFGLGGLGQVGSHEFLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
 DB 1 MAPLGEVNGFVGQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54
 QY 58 AHLHGILRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
 DB 55 DHLKGLILRRRLQYCRGTGFHLEIFPNGTIOGTRKDHRSRFGILEFISIAVGLVSRGVDSGL 114
 QY 118 YLGMNDKGLYSGEKLISECIRFQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPTD 177
 DB 115 YLGMNEKGLYSGEKLITQECVFRQFEENWNTYSSNLYKHVDTRRRYFVALNKDGTPTRE 174
 QY 178 GASKRKHQKFTFLPRPVDPRVPELYKDIL 208
 DB 175 GTRTKRKHQKFTFLPRPVDPKVPELYKDIL 205

RESULT 13
 AAW11547
 ID AAW11547 standard; Protein; 208 AA.
 XX
 AC AAW11547;
 XX
 DT 17-SEP-1997 (first entry)
 XX
 DE Amino acid sequence of mouse FGF9 encoded by FGF9:pET-3C.
 XX
 KW Mouse; chicken; fibroblast growth factor 9; FGF9; detection;
 KW fibroblast growth factor receptor 3; FGFR3; cartilage repair;
 KW bone repair; antagonist; anti-FGF9 antibody; endochondromas;

KW solitary hereditary exostosis; multiple hereditary exostosis;
 KW hallux valgus deformity; achondroplasia; synovial chondromatosis.
 XX
 OS Mus musculus.
 XX
 PN W09641523-A1.
 XX
 PD 27-DEC-1996.
 XX
 PF 12-JUN-1996; 96WO-IL00011.
 XX
 PR 12-JUN-1995; 95US-0000137.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Yayon A;
 XX
 DR WPI; 1997-065215/06.
 XX
 DR N-PSDB; AAT58530.
 XX
 PT Medical and diagnostic use of fibroblast growth factor 9 - and
 PT recombinant fibroblast growth factor 9 DNA
 XX
 PS Claim 12; Fig 1; 32pp; English.
 XX
 CC The sequences given in AAW11547-48 represent mouse and chicken
 CC fibroblast growth factor 9 (FGF9), respectively. FGF9 may be used in the
 CC method of the invention for detecting fibroblast growth factor receptor 3
 CC (FGFR3) in a sample or tissue. The method comprises contacting the
 CC sample or tissue with FGF9, allowing formation of receptor-ligand pairs,
 CC and detecting any FGFR3-FGF9 pairs. Compositions containing FGF9 can
 CC be used to increase FGFR3 activity, esp. to stimulate cartilage or bone
 CC repair. Compositions containing FGF9 antagonists or FGF9 binding agents
 CC (e.g. anti-FGF9 antibodies) can be used to treat diseases caused by an
 CC excess of FGF9 or overactivity of FGFR3, esp. multiple or solitary
 CC hereditary exostosis, hallux valgus deformity, achondroplasia, synovial
 CC chondromatosis and endochondromas.
 XX
 SQ Sequence 208 AA;
 Query Match 69.3%; Score 774.5; DB 18; Length 208;
 Best Local Similarity 70.6%; Pred. No. 1.5e-74;
 Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFGLGGLGQVGSHEFLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
 DB 1 MAPLGEVNGFVGQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54
 QY 58 AHLHGILRRRLQYCRGTGFHLQILPDGVSQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
 DB 55 DHLKGLILRRRLQYCRGTGFHLEIFPNGTIOGTRKDHRSRFGILEFISIAVGLVSRGVDSGL 114
 QY 118 YLGMNDKGLYSGEKLISECIRFQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPTD 177
 DB 115 YLGMNEKGLYSGEKLITQECVFRQFEENWNTYSSNLYKHVDTRRRYFVALNKDGTPTRE 174
 QY 178 GASKRKHQKFTFLPRPVDPRVPELYKDIL 208
 DB 175 GTRTKRKHQKFTFLPRPVDPKVPELYKDIL 205

RESULT 14
 AAW75719
 ID AAW75719 standard; Protein; 208 AA.
 XX
 AC AAW75719;
 XX
 DT 07-DEC-1998 (first entry)
 XX
 DE Fibroblast growth factor-9.
 XX
 KW Fibroblast growth factor-9; FGF-9; mutein; protein engineering;
 KW heparin; thrombosis; thrombocytopenia; ophthalmic disorder;


```

Db      175  GTRTKRHKQKFTHELPRVDPDKVPELYKDIL  205
      | | : | | | | | | | | | | : | | | | | : |

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Search completed: October 21, 2002, 16:14:15
Job time : 33 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:13:40 ; Search time 13 seconds
(without alignments)
396.446 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 1118

Sequence: 1 MAPLAEVGGFLGGLGQQ.....PRVPDPERVPELYKDLIMYT 211

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	774.5	69.3	208	1	US-08-340-820-3
2	774.5	69.3	208	1	US-08-340-820-9
3	774.5	69.3	208	1	US-08-340-820-25
4	774.5	69.3	208	1	US-08-172-328-3
5	774.5	69.3	208	1	US-08-593-535-3
6	774.5	69.3	208	1	US-08-593-535-9
7	774.5	69.3	208	1	US-08-593-535-25
8	774.5	69.3	208	1	US-08-439-725A-7
9	774.5	69.3	208	1	US-08-462-169B-17
10	774.5	69.3	208	2	US-08-207-412B-13
11	774.5	69.3	208	2	US-08-867-471-7
12	774.5	69.3	208	2	US-08-438-439C-12
13	774.5	69.3	208	2	US-08-951-822-34
14	774.5	69.3	208	2	US-08-943-915-3
15	774.5	69.3	208	3	US-09-103-079-17
16	774.5	69.3	208	3	US-08-705-245-7
17	774.5	69.3	208	3	US-08-718-904-18
18	774.5	69.3	208	3	US-09-023-082A-18
19	774.5	69.3	208	4	US-09-368-951-34
20	769.5	68.8	207	1	US-08-340-820-2
21	769.5	68.8	207	1	US-08-172-328-2
22	769.5	68.8	207	1	US-08-593-535-2
23	769.5	68.8	208	1	US-08-464-590A-10
24	769.5	68.8	208	3	US-09-093-585-10
25	769.5	68.8	205	1	US-08-340-820-5
26	758.5	67.8	205	1	US-08-172-328-4
27	758.5	67.8	205	1	US-08-593-535-5

28	758.5	67.8	206	1	US-08-340-820-7	Sequence 7, Appli
29	758.5	67.8	206	1	US-08-340-820-8	Sequence 8, Appli
30	758.5	67.8	206	1	US-08-172-328-5	Sequence 5, Appli
31	758.5	67.8	206	1	US-08-593-535-7	Sequence 7, Appli
32	758.5	67.8	206	1	US-08-593-535-8	Sequence 8, Appli
33	742	66.4	175	1	US-08-172-328-6	Sequence 6, Appli
34	742	66.4	176	1	US-08-172-328-7	Sequence 7, Appli
35	742	66.4	177	1	US-08-340-820-4	Sequence 4, Appli
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38	742	66.4	178	1	US-08-593-535-6	Sequence 6, Appli
39	729	65.2	159	1	US-08-172-328-8	Sequence 8, Appli
40	729	65.2	160	1	US-08-172-328-9	Sequence 9, Appli
41	710.5	63.6	193	2	US-08-438-439C-21	Sequence 21, Appli
42	708.5	63.4	207	2	US-08-943-915-5	Sequence 5, Appli
43	705.5	63.1	207	2	US-08-943-915-2	Sequence 2, Appli
44	702.5	62.8	190	1	US-08-441-629-16	Sequence 16, Appli
45	702.5	62.8	190	3	US-08-776-207-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-340-820-3
; Sequence 3, Application US/08340820
; Patent No. 5512460
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/835,713
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-340-820-3

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;


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QY 1 MAPLAEVGGFLGGLGQQVGSFHLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
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Db 1 MAPLGEVGNVFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54

QY 58 AHLHGILRRRLQYCRTHGHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDSGL 117
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Db 55 DHLGKILRRRLQYCRTHGHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDSGL 114

QY 118 YLGMNDKGLYSGKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPTD 177
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 YLGMNEKGLYSGKLTQECVFRQFEENWNTYSSNLYKHVDTRRRYYVALNKDGTPTRE 174

QY 178 GARSKRHQKTHFLPRPVDPERVPELYKDIL 208
| : ||||| : : : : : : : : : : : : : : : : : : : : : : :
Db 175 GTRTKRHQKTHFLPRPVDPKVPELYKDIL 205
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RESULT 4

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US-08-172-328-3
; Sequence 3, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIODIES, POLYPEPTIDES, PRODUCTION AND
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
US-08-172-328-3
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Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;

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Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;
QY 1 MAPLAEVGGFLGGLGQQVGSFHLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAPLGEVGNVFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54

QY 58 AHLHGILRRRLQYCRTHGHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDSGL 117
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 DHLGKILRRRLQYCRTHGHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDSGL 114

QY 118 YLGMNDKGLYSGKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPTD 177
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 YLGMNEKGLYSGKLTQECVFRQFEENWNTYSSNLYKHVDTRRRYYVALNKDGTPTRE 174

QY 178 GARSKRHQKTHFLPRPVDPERVPELYKDIL 208
| : ||||| : : : : : : : : : : : : : : : : : : : : : : :
Db 175 GTRTKRHQKTHFLPRPVDPKVPELYKDIL 205
```

RESULT 5

```
US-08-593-535-3
; Sequence 3, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-593-535-3
```

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;

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Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;
QY 1 MAPLAEVGGFLGGLGQQVGSFHLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
||||| : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAPLGEVGNVFGVQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54
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QY 58 AHLHGILRRRLCYCRTGFHLLQILPDGSGVQCTRODHSLSFGILEFTSVAVLVSIRGVDSGL 117
DB 55 DHLAKGILRRRLCYCRTGFHLEIFPNGTIOGTRKDHRSRFGILEFTSIAVLVSIRGVDSGL 114
QY 118 YLGMNDKGLYSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRD 177
DB 115 YLGMNEKGLYSEKLTQECVFEQFEENWNTYSSNLYKHVDTHGRRYYVALNKDGTPRE 174
QY 178 GARSKRHQKFTHFLPRPDPKVPPELYKDIL 208
DB 175 GTRTKRHOKEFTHFLPRPDPKVPPELYKDIL 205

RESULT 6
US-08-593-535-9
; Sequence 9, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-593-535-9
Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGFLGLEGLGQGVSHFLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
DB 1 MAPLGEVGNVFGQDAV--PFGNVPLPV--DSPVLLSDHLGQSE--AGGLPRGPVAVTDL 54
QY 58 AHLHGILRRRLCYCRTGFHLLQILPDGSGVQCTRODHSLSFGILEFTSVAVLVSIRGVDSGL 117
DB 55 DHLAKGILRRRLCYCRTGFHLEIFPNGTIOGTRKDHRSRFGILEFTSIAVLVSIRGVDSGL 114

QY 118 YLGMNDKGLYSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRD 177
DB 115 YLGMNEKGLYSEKLTQECVFEQFEENWNTYSSNLYKHVDTHGRRYYVALNKDGTPRE 174
QY 178 GARSKRHQKFTHFLPRPDPKVPPELYKDIL 208
DB 175 GTRTKRHOKEFTHFLPRPDPKVPPELYKDIL 205

RESULT 7
US-08-593-535-25
; Sequence 25, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: skin
; CELL TYPE: fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pcAFL
; US-08-593-535-25

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGFLGLEGLGQGVSHFLPPAGERPPLLGERRSAAERSARG---GPGAAQL 57
DB 1 MAPLGEVGNVFGQDAV--PFGNVPLPV--DSPVLLSDHLGQSE--AGGLPRGPVAVTDL 54

RESULT 9
US-08-462-169B-17
; Sequence 17, Application US/08462169B
; Patent No. 5773252
; GENERAL INFORMATION:
; APPLICANT: John Greene and Craig A. Rosen
; TITLE OF INVENTION: Fibroblast Growth Factor-15

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Query Match      69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY  1 MAPLAEVGGFLGLEGLOGOVGSHFLLPPAGERPPLIGERRSAERSARG--GPGAAQL 57
      ||||| ||||| : : : : || : : : : : : : : : : : : : : :
Db  1 MAPLGEVGNFVGQDAV--PFGNVPLBV--DSPVLLSDHLGQSE--AGGLPRGPVATDL 54
      ||||| ||||| : : : : || : : : : : : : : : : : : : : :

QY  58 AHLHGILRRRQLYCRGFHLQLPDCSVQGRQDHSFLGLEFISAVGLSVRGVDSGL 117
      ||||| ||||| : : : : || : : : : : : : : : : : : : : :
Db  55 DHLKGLILRRRQLYCRGFHLEIFPNGTQTGRKDSRFGILLEFISIAVGLSVRGVDSGL 114
      ||||| ||||| : : : : || : : : : : : : : : : : : : : :

QY  118 YLGWMDKGELYSEKUTSICIFREQFEENWNTYSSNIYKHGDGRRYFVALNKDGTPRD 177
      ||||| ||||| : : : : || : : : : : : : : : : : : : : :
Db  115 YLGWMDKGELYSEKUTSICVREQFEENWNTYSSNIYKHVDGRRYFVALNKDGTGRE 174
      ||||| ||||| : : : : || : : : : : : : : : : : : : : :

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RESULT 10
US-08-207-412B-13
; Sequence 13, Application US/08207412B
; Patent No. 5817485
; GENERAL INFORMATION:
; APPLICANT: Hu, Jing-Shan
; TITLE OF INVENTION: Fibroblast Growth Factor-10

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RESULT 15
US-09-103-079-17
; Sequence 17 Application US/09103079A
; Patent No. 6013477
; GENERAL INFORMATION:
; APPLICANT: Greene, John M.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: Fibroblast Growth Factor 15
; FILE REFERENCE: PF203D1
; CURRENT APPLICATION NUMBER: US/09/103,079A
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 08/462,169
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-079-17

Query Match      69.3%; Score 774.5; DB 3; Length 208;
Best Local Similarity 70.6%; Pred. No. 2e-79;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEVGGFLGGLGQQVGSFLLPPAGERPPLLGERSSAERSARC---GPGAAQL 57
Db 1 MAPGEVGNVFGVQDAV--PFGNVPLPV--DSPVLLSDHLGQSE--AGGLPRGPVTDL 54

QY 58 AHLHGILRRRLQYCRGTFHQLIPDGSVQGTRODHSLEFISVAVGLSVIRGVDSGL 117
Db 55 DHLKGILRRRLQYCRGTFHLEIFPNGTIQTRKDSRFGILEFISIAVGLSVIRGVDSGL 114

QY 118 YLGMNDKGELYGSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRD 177
Db 115 YLGMNEKGELYGSEKLTQECVFRQFEENWNTYSSNLYKHVDTGRRYVVALNKDGTPRE 174

QY 178 GARSRRHOKFTFLPRPVDPERVPKDL 208
Db 175 GTTRKRHOKFTFLPRPVDPKVPKDL 205

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Search completed: October 21, 2002, 16:15:54
Job time : 14 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 21, 2002, 16:12:50 ; Search time 21 Seconds
(without alignments)
965.469 Million cell updates/sec

Title: US-09-817-814-2
Perfect score: 1118
Sequence: 1 MAPLAEVGGFLGGLEGLGQQ.....PRPVDPERVELYKDLLMYT 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	100.0	211	2 JC7353	fibroblast growth
2	1074	96.1	212	2 JC7511	fibroblast growth
3	904.5	80.9	208	2 JC7082	fibroblast somatot
4	774.5	69.3	208	2 S66486	fibroblast growth
5	774.5	69.3	208	2 A48137	fibroblast growth
6	708.5	63.4	207	2 JC5941	fibroblast growth
7	705.5	63.1	207	2 JC5940	fibroblast growth
8	342.5	30.6	220	2 I50588	fibroblast growth
9	324.5	29.0	266	2 S68144	fibroblast growth
10	324	29.0	237	1 S39582	transforming prote
11	324	29.0	267	1 TVHUP5	fibroblast growth
12	321	28.7	264	2 A36207	fibroblast growth
13	319	28.5	239	1 S04742	fibroblast growth
14	317	28.4	245	1 TVMST2	transforming prote
15	307	27.5	256	2 JC4627	fibroblast growth
16	297	26.6	194	2 S26049	fibroblast growth
17	292	26.1	194	2 I48610	fibroblast growth
18	290	25.9	194	1 A36301	keratinocyte growt
19	290	25.9	194	2 S49501	fibroblast growth
20	289	25.8	168	2 JG0184	keratinocyte growt
21	288.5	25.8	194	2 I50710	fibroblast growth
22	282.5	25.3	208	2 S20102	fibroblast growth
23	281.5	25.2	208	2 S14192	fibroblast growth
24	279.5	25.0	187	2 S23595	embryonic fibrobla
25	278	24.9	413	2 H88481	protein let-756 [i
26	275	24.6	206	2 JC4268	fibroblast growth
27	270	24.2	206	1 TVHUHS	fibroblast growth
28	268.5	24.0	192	2 S54407	embryonic fibrobla
29	256	22.9	155	1 A60721	acidic fibroblast

30	256	22.9	202	1 TVMSHS	fibroblast growth
31	255	22.8	152	2 JH0476	acidic fibroblast
32	254.5	22.8	155	2 S04147	acidic fibroblast
33	254.5	22.8	155	2 D37360	acidic fibroblast
34	251	22.5	155	1 A33665	acidic fibroblast
35	243.5	21.8	155	2 A60130	acidic fibroblast
36	235.5	21.1	155	2 JW0055	acidic fibroblast
37	234.5	21.0	155	1 GKBOA	acidic fibroblast
38	218.5	19.5	210	2 A32398	basic fibroblast g
39	214	19.1	97	2 B46289	keratinocyte growt
40	213	19.1	98	2 C46289	keratinocyte growt
41	211.5	18.9	189	2 A48834	basic fibroblast g
42	209	18.7	157	1 GKBOB	basic fibroblast g
43	205	18.3	154	2 A31674	basic fibroblast g
44	204.5	18.3	154	2 C37360	basic fibroblast g
45	204.5	18.3	164	2 S31622	basic fibroblast g

ALIGNMENTS

RESULT 1
JC7353
fibroblast growth factor-20 - human
C:Species: Homo sapiens (man)
C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 01-Dec-2000
C:Accession: JC7353
R:Kirikoshi, H.; Sagara, N.; Saitoh, T.; Tanaka, K.; Sekihara, H.; Shiohara, K.; Kato
Biochem. Biophys. Res. Commun. 274, 337-343, 2000
A:Title: Molecular cloning and characterization of human FGF-20 on chromosome 8p21.3-
A:Reference number: JC7353
A:Accession: JC7353
A:Molecule type: mRNA
A:Residues: 1-211 <KIR>
A:Cross-references: DDBJ:AB044277
C:Comment: This factor is involved in physiological and pathological processes, play
C:Genetics:
A:Gene: fgf-20
A:Map position: 8p21.3-8p22
C:Superfamily: fibroblast growth factor
C:Keywords: angiogenesis; carcinogenesis

Query Match	100.0%	Score 1118;	DB 2;	Length 211;
Best Local Similarity	100.0%;	Pred. No. 1.3e-97;		
Matches 211;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAPLAEVGGFLGGLEGLGQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL	60	
Db	1	MAPLAEVGGFLGGLEGLGQVGSFLLPPAGERPPLLGERRSAAERSARGGPGAAQLAHL	60	
QY	61	HGILRRQLYCRGFHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDSGLYLG	120	
Db	61	HGILRRQLYCRGFHLQILPDGSGVQGTQDHSFLGILEFISVAVGLSVIRGVDSGLYLG	120	
QY	121	MNDKGELYSEKLTSCIFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTTPRDGAR	180	
Db	121	MNDKGELYSEKLTSCIFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTTPRDGAR	180	
QY	181	SKRHQKTFHFLPRPVDPERVPELYKDLLMYT	211	
Db	181	SKRHQKTFHFLPRPVDPERVPELYKDLLMYT	211	

RESULT 2
JC7511
fibroblast growth factor-20 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7511
R:Ohmachi, S.; Watanabe, Y.; Mikami, T.; Kusu, N.; Ibi, T.; Akaike, A.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 355-360, 2000
A:Title: FGF-20, a novel neurotrophic factor, preferentially expressed in the substan
A:Reference number: JC7511; MUID:20490008

Db 115 YLGMNEKGLYSGSEKLTQECVFEQFENNYNTYSSNLYKHVDTGRRYVVALNKDGTGRE 174

QY 178 GASKRHOKFTHELPRVDPDPVPELYKDIL 208

Db 175 GTRKRHOKFTHELPRVDPDPVPELYKDIL 205

RESULT 6

JC5941

fibroblast growth factor 16 - human

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: JC5941

R: Miyake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami, Biochem. Biophys. Res. Commun. 243, 148-152, 1998

A:Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor family

A:Reference number: JC5940; MUID:98139883

A:Accession: JC5941

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-207 <Miy>

A:Cross-references: DDBJ:AB009391; NID:g29111169; PIDN:BAA24956.1; PID:g29111170

C:Superfamily: fibroblast growth factor

Query Match 63.4%; Score 708.5; DB 2; Length 207;

Best Local Similarity 63.2%; Pred. No. 3.8e-59;

Matches 134; Conservative 27; Mismatches 40; Indels 11; Gaps 4;

QY 4 LAEYGGFLGG-----GLGQQVGSFHELLPPAGERPPLGERRSAE--RSARGGPGAAQLA 58

Db 1 MAEYGGVFASLDWDLHGFSLSGN---VPLADSPGFLNERLQIEGKLQRGSP--TDFA 54

QY 59 HLHGILRRRLQYCRTHFLQILPDGSGVQGTRODHSFLGILEFISVAVGLVSRIGVDSGLY 118

Db 55 HLKGLRRRLQYCRTHFLQILPDGSGVQGTRODHSFLGILEFISVAVGLVSRIGVDSGLY 114

QY 119 LGMNDKGLYSGSEKLTQECVFEQFENNYNTYSSNLYKHVDTGRRYVVALNKDGTGRE 178

Db 115 LGMNEKGLYSGSEKLTQECVFEQFENNYNTYSSNLYKHVDTGRRYVVALNKDGSPPREG 174

QY 179 ARSKRHOKFTHELPRVDPDPVPELYKDILMY 210

Db 175 YTRKRHOKFTHELPRVDPDPVPELYKDILMY 206

RESULT 7

JC5940

fibroblast growth factor 16 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: JC5940

R: Miyake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami, Biochem. Biophys. Res. Commun. 243, 148-152, 1998

A:Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor family

A:Reference number: JC5940; MUID:98139883

A:Accession: JC5940

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-207 <Miy>

A:Cross-references: DDBJ:AB002561; NID:g29111149; PIDN:BAA24947.1; PID:g29111150

C:Superfamily: fibroblast growth factor

Query Match 63.1%; Score 705.5; DB 2; Length 207;

Best Local Similarity 62.7%; Pred. No. 7.3e-59;

Matches 133; Conservative 28; Mismatches 40; Indels 11; Gaps 4;

QY 4 LAEYGGFLGG-----LEGGLQVGSFHELLPPAGERPPLGERRSAE--RSARGGPGAAQLA 58

Db 1 MAEYGGVFASLDWDLQGFSSLSGN---VPLADSPGFLNERLQIEGKLQRGSP--TDFA 54

QY 59 HLHGILRRRLQYCRTHFLQILPDGSGVQGTRODHSFLGILEFISVAVGLVSRIGVDSGLY 118

Db 55 HLKGLRRRLQYCRTHFLQILPDGSGVQGTRODHSFLGILEFISVAVGLVSRIGVDSGLY 114

QY 119 LGMNDKGLYSGSEKLTQECVFEQFENNYNTYSSNLYKHVDTGRRYVVALNKDGTGRE 178

Db 115 LGMNEKGLYSGSEKLTQECVFEQFENNYNTYSSNLYKHVDTGRRYVVALNKDGSPPREG 174

QY 179 ARSKRHOKFTHELPRVDPDPVPELYKDILMY 210

Db 175 YTRKRHOKFTHELPRVDPDPVPELYKDILMY 206

RESULT 8

I50588

fibroblast growth factor 3 - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 17-Mar-2000

C:Accession: I50588

R: Mahmood, R.; Kiefer, P.; Guthrie, S.; Dickson, C.; Mason, I. Development 121, 1399-1410, 1995

A:Title: Multiple roles for FGF-3 during cranial neural development in the chicken.

A:Reference number: I50588; MUID:95309122

A:Accession: I50588

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-220 <MAH>

A:Cross-references: EMBL:Z47555; NID:g623215; PIDN:CAA87635.1; PID:g623216

C:Superfamily: fibroblast growth factor

Query Match 30.6%; Score 342.5; DB 2; Length 220;

Best Local Similarity 41.6%; Pred. No. 1e-24;

Matches 77; Conservative 29; Mismatches 56; Indels 23; Gaps 4;

QY 26 LLP-----PAGERPPLGERRSAERSARGGPGAAQLAHLHGILRRRLQYCRTHFLQILP 81

Db 11 LLPERPVPATASP-----RAPRDAGRGG-----VYELGGAPRRKKLYCATKYHLQIHP 61

QY 82 DGSVQGTRODHSFLGILEFISVAVGLVSRIGVDSGLYLCMNDKGLYSEKLTSECFIRE 141

Db 62 GKGINGTLEKNSVFSILEITAVDVGIVAKGLFSGRYLAMNKRGLYASENYNTCEFEVE 121

QY 142 QFENNYNTYSSNLYKHVDTG-----RRYFVALNKDGTGREARSKRHOKFTHFL 191

Db 122 RIHELGYNTYASRLYRTVPVSGASTKKASAEKRLWYVSVNGRPRRGFKTRTKSSLFL 181

QY 192 PREVD 196

Db 182 PRVLD 186

RESULT 9

S68144

fibroblast growth factor 5 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

C:Accession: S68144

R: Hattori, Y.; Yamasaki, M.; Itoh, N. Biochim. Biophys. Acta 1306, 31-33, 1996

A:Title: The rat FGF-5 mRNA variant generated by alternative splicing encodes a novel

A:Reference number: S68144; MUID:96201703

A:Accession: S68144

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-266 <HAT>

A:Cross-references: EMBL:D64085; NID:g992952; PIDN:BAA10966.1; PID:g992953

C:Superfamily: fibroblast growth factor

Query Match 29.0%; Score 324.5; DB 2; Length 266;

Best Local Similarity 39.8%; Pred. No. 6.6e-23;

Matches 86; Conservative 24; Mismatches 69; Indels 37; Gaps 9;

QY 23 SHFLL--PPAGER-----PP-----LLGER-----RSAERSARGGPGAAQLA 58

Db 12 SHLLSAPAGEKRLTPEGQAPPPRNPNGSSGSRGSSATFASSASSPVAASPGSGG 71

N:Alternate names: transforming protein int-2
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C:Accession: S04742
R:Brookes, S.; Smith, R.; Casey, G.; Dixon, M.; Peters, G.
Oncogene 4, 429-436, 1989
A:Title: Sequence organization of the human int-2 gene and its expression in teratocarcinoma
A:Reference number: S04742; MUID:89239468
A:Accession: S04742
A:Molecule type: DNA
A:Residues: 1-239 <BROS>
A:Cross-references: EMBL:X14445; NID:g33937; PIDN:CAA32615.1; PID:g312409
C:Genetics:
A:Gene: GDB:FGF3; INT2
A:Cross-references: GDB:120103; OMIM:164950
A:Map position: 11q13.3-11q13.3
A:Introns: 74/1; 108/3
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-239/Product: transforming protein (int-2) #status predicted <MAT>

Query Match 28.5%; Score 319; DB 1; Length 239;
Best Local Similarity 41.1%; Pred. No. 1.9e-22;
Matches 78; Conservative 29; Mismatches 61; Indels 22; Gaps 6;

QY 28 PPAGERPPILLGERRSAERSARGGGAQAHLHGLRRRLRYCRTGFHLQILPDGSGVQG 87
Db 17 PAAGPGARL---RRDA-----GGRGV-YEHLGGAPRRKLYCATYHQLHPSGRVNG 66

QY 88 TRODHLGFLGIFISVAVGLVIRGVDGLYGMNDKGLYSEKLTSECFRFEENW 147
Db 67 S-LENSAYSILEITAVEGIVAIRGLFSGRVLANMKRGLYASAECEFEVERIHELG 125

QY 148 YNTYSSNIY-----KHGDTGRRYFVALNKDGTDPDGAARKHOKFTFHLPRVDP 197
Db 126 YNTYASRLYRTVSTPGARRQPSAERLWYVSVNGKGRPRGFKTRTQKSLFLPRVLD- 184

QY 198 ERVPELYKDL 207
Db 185 HRDHEWVRQL 194

RESULT 14
TVMST2
A:Title: transforming protein (int-2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 18-Jun-1999
C:Accession: A23930; S08157
R:Moore, R.; Casey, G.; Brookes, S.; Dixon, M.; Peters, G.; Dixon, C.
EMBO J. 5, 919-924, 1986
A:Title: Sequence, topography and protein coding potential of mouse int-2: a putative on-
cogene
A:Reference number: A23930; MUID:86247582
A:Accession: A23930
A:Molecule type: DNA; mRNA
A:Residues: 1-245 <MOO>
A:Cross-references: GB:Y00848; GB:X68450; NID:g52716; PIDN:CAAG68767.1; PID:g52716
R:Acland, P.; Dixon, M.; Peters, G.; Dixon, C.
Nature 343, 662-665, 1990
A:Title: Subcellular fate of the Int-2 oncoprotein is determined by choice of initiation
A:Reference number: S08157; MUID:90158795
A:Accession: S08157
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 'HSRAGLARGVLPAPRLRETRAGAAAAGGRDAGM', 3-17 <ACL>
C:Genetics:
A:Gene: int-2
A:Map position: 7
A:Introns: 74/1; 108/3
C:Superfamily: fibroblast growth factor
C:Keywords: growth factor; transforming protein

Query Match 28.4%; Score 317; DB 1; Length 245;

Best Local Similarity 43.0%; Pred. No. 3e-22;
Matches 68; Conservative 28; Mismatches 50; Indels 12; Gaps 3;

QY 46 REARGPGAAQLAHLHGLRRRLRYCRTGFHLQILPDGSGVOGTRODHSLEIFTSVAV 105
Db 26 RRDAGRGV-YEHLGGAPRRKLYCATYHQLHPSGRVNGS-LENSAYSILEITAVEV 83

QY 106 GLVSRGVDSGLYGMNDKGLYSEKLTSPCIFRFEENWYNTYSSNIYKHGDTG--- 162
Db 84 GVVAIKGLFSGYLANMKRGLYASDHYNACEFEVERIHELGYNTYASRLYRIGSSGPGA 143

QY 163 -----RRYFVALNKDGTDPDGAARKHOKFTFHLPR 193
Db 144 QRQGAORPWYVSVNGKGRPRGFKTRTQKSLFLPR 181

RESULT 15
JC4627
A:Title: fibroblast growth factor 3 - zebra fish
C:Species: Brachydanio rerio (zebra fish)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 16-Jul-1999
C:Accession: JC4627
R:Kiefer, P.; Straehle, U.; Dickson, C.
Gene 168, 211-215, 1996
A:Title: The zebrafish Fgf-3 gene: cDNA sequence, transcript structure and genomic or-
ganization
A:Reference number: JC4627; MUID:96194899
A:Accession: JC4627
A:Molecule type: mRNA
A:Residues: 1-256 <KIE>
A:Cross-references: EMBL:Z48714; NID:g971333; PIDN:CAA88596.1; PID:g971334
A:Experimental source: embryo
A:Note: The authors translated the codon TGG for residue 178 as His
C:Comment: This factor belongs to the fibroblast growth factor family which have the
protein is a cell signalling molecule and plays the roles during the early stages of de-
velopment
A:Gene: Fgf-3
A:Introns: 93/2; 127/3
C:Superfamily: fibroblast growth factor
C:Keywords: embryo; fibroblast; growth factor

Query Match 27.5%; Score 307; DB 2; Length 256;
Best Local Similarity 37.0%; Pred. No. 2.8e-21;
Matches 70; Conservative 33; Mismatches 66; Indels 20; Gaps 3;

QY 34 PELLGERRSAERSARGGGAQAHLHGLRRRLRYCRTGFHLQILPDGSGVOGTRODHS 93
Db 32 PCARGQACDPQRORDAGRGV-YEHLGGAPRRKLYCATYHQLHPSGRVNGSLENN 90

QY 94 LFGILEFTSVAVGLVIRGVDGLYGMNDKGLYSEKLTSECFRFEENWYNTYSS 153
Db 91 PLSILEITAVDGVVAIKGLFSGRVLANMKRGLYASDHYNACEFEVERIHELGYNTYAS 150

QY 154 NIY-----KHGDTGRRYFVALNKDGTDPDGAARKHOKFTFHLPRV-- 195
Db 151 RHHATTQPPPTGGGIGGSKRRASSKRWVSVNGKGRPRGFKTRTQKSLFLPRVLN 210

QY 196 -DPERVPEL 203
Db 211 KOHEMWVRKL 219

Search completed: October 21, 2002, 16:15:34
Job time : 22 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:10:10 ; Search time 12 Seconds
(without alignments)
680.819 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 1118

Sequence: 1 MAPLAEVGGFLGGLGCGQ.....PRVDPVRVPELYKDLIMYT 211

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1118	100.0	211	1	FGPK_HUMAN
2	774.5	69.3	208	1	FGF9_HUMAN
3	774.5	69.3	208	1	FGF9_MOUSE
4	774.5	69.3	208	1	FGF9_RAT
5	765	68.4	209	1	FGF9_XENLA
6	708.5	63.4	207	1	FGFG_HUMAN
7	705.5	63.1	207	1	FGFG_RAT
8	342.5	30.6	220	1	FGF3_CHICK
9	324.5	29.0	266	1	FGF5_RAT
10	324	29.0	237	1	FGF3_XENLA
11	322.5	28.8	268	1	FGF5_HUMAN
12	322	28.8	162	1	FGPM_MOUSE
13	321	28.7	264	1	FGF5_MOUSE
14	319	28.5	239	1	FGF3_HUMAN
15	317	28.4	245	1	FGF3_MOUSE
16	312	28.0	247	1	FGFE_HUMAN
17	312	27.9	247	1	FGFE_MOUSE
18	308	27.5	208	1	FGFA_HUMAN
19	308	27.5	215	1	FGFA_RAT
20	307	27.5	170	1	FGFM_HUMAN
21	307	27.5	256	1	FGF3_BRARE
22	301.5	27.0	245	1	FGFD_MOUSE
23	300.5	26.9	245	1	FGFD_HUMAN
24	297	26.6	209	1	FGFA_MOUSE
25	292	26.1	194	1	FGF7_CANFA
26	292	26.1	194	1	FGF7_MOUSE
27	292	26.1	194	1	FGF7_RAT
28	292	26.1	243	1	FGFC_HUMAN
29	290	25.9	194	1	FGF7_HUMAN
30	290	25.9	194	1	FGF7_SHEEP
31	288.5	25.8	194	1	FGF4_CHICK
32	282.5	25.3	208	1	FGF6_HUMAN
33	281.5	25.2	208	1	FGF6_MOUSE

34	279.5	25.0	187	1	FGFA_XENLA
35	279	25.0	194	1	FGF7_PIG
36	278.5	24.9	225	1	FGFB_HUMAN
37	278	24.9	413	1	L756_CAEEL
38	271.5	24.3	225	1	FGFB_MOUSE
39	270	24.2	206	1	FGF4_HUMAN
40	269	24.1	206	1	FGF4_BOVIN
41	268.5	24.0	192	1	FGFB_XENLA
42	256	22.9	155	1	FGFL_MESAU
43	256	22.9	202	1	FGF4_MOUSE
44	255	22.8	152	1	FGFL_PIG
45	254.5	22.8	155	1	FGFL_MOUSE

ALIGNMENTS

RESULT 1

FGFK_HUMAN

ID FGFK_HUMAN STANDARD; PRT; 211 AA.

AC Q9NFP95;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Fibroblast growth factor-20 (FGF-20).

GN FGF20.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20374469; PubMed=10913340;

RA Kirikoshi H., Sadara N., Saiton T., Tanaka K., Sekihara H.,

RA Shioikawa K., Katoh M.;

RT "Molecular cloning and characterization of human FGF-20 on chromosome

8p21.3-p22.;"

RL Biochem. Biophys. Res. Commun. 274:337-343(2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Itoh N.;

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.

CC -----
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DR EMBL; AB044277; BAB03633.1; -

DR EMBL; AB030648; BAB03530.1; -

DR MIM; 605558;

DR InterPro; IPR002209; HBGFG_FGF.

DR InterPro; IPR002348; ILJ_HBGF.

DR Pfam; PF00167; FGF; 1.

DR PRINTS; PR00262; ILI1HBGF.

DR ProDom; PD000831; HBGFG_FGF; 1.

DR SMART; SM00442; FGF; 1.

DR PROSITE; PS00247; HBGFG_FGF; 1.

KW Growth factor.

SQ SEQUENCE 211 AA; 23498 MW; AB04608C16060CC1 CRC64;

Query Match 100.0%; Score 1118; DB 1; Length 211;

Best Local Similarity 100.0%; Pred. No. 1.4e-97;

Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPLAEVGGFLGGLGCGQVSHFLLPPAGERPPLLGKRSAAERSARGGPGGAQLAHL 60

|||||

1 MAPLAEVGGFLGGLGCGQVSHFLLPPAGERPPLLGKRSAAERSARGGPGGAQLAHL 60

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QY 61 HGILRRRLCYRTGFHLQILPDGSGVOGTRODHSFGILEFTISVAVGLVSTIRGVDSGLYL 120
Db 61 HGILRRRLCYRTGFHLQILPDGSGVOGTRODHSFGILEFTISVAVGLVSTIRGVDSGLYL 120
QY 121 MNDKGLYSGSEKLTSECIFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGR 180
Db 121 MNDKGLYSGSEKLTSECIFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGR 180
QY 181 SKRHQKFTFLPRVDPVPELVKDLMLMT 211
Db 181 SKRHQKFTFLPRVDPVPELVKDLMLMT 211

RESULT 2
FGF9_HUMAN
ID FGF9_HUMAN STANDARD; PRT; 208 AA.
AC P31371;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).
GN FGF9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Foreskin;
RX MEDLINE=93309459; PubMed=8321227;
RA Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
RA Kurokawa T.;
RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
RT of the fibroblast growth factor family, which has a unique secretion
RT property.";
RL Mol. Cell. Biol. 13:4251-4259(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Blakey S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 4-26 AND 34-54.
RC TISSUE=Glia; tumor;
RX MEDLINE=93155105; PubMed=8428960;
RA Naruo K.-I., Seko C., Kuroshima K.-I., Matsutani E., Sasada R.,
RA Kondo T., Kurokawa T.;
RT "Novel secretory heparin-binding factors from human glioma cells
RT (glia-activating factors) involved in glial cell growth.
RT Purification and biological properties.";
RL J. Biol. Chem. 268:2857-2864(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.60 ANGSTROMS).
RX MEDLINE=21127675; PubMed=11223514;
RA Hecht H.J., Adar R., Hofmann B., Bogin O., Welch H., Yayon A.;
RT "Structure of fibroblast growth factor 9 shows a symmetric dimer with
RT unique receptor- and heparin-binding interfaces.";
RL Acta Crystallogr. D 57:378-384(2001).
CC -1- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLIOSIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: GLIAL CELLS.
CC -1- PTM: THREE MOLECULAR SPECIES WERE FOUND (30 KDA, 29 KDA AND 25
CC KDA), CLEAVED AT LEU-4, VAL-13 AND SER-34 RESPECTIVELY. THE
CC SMALLER ONES MIGHT BE PRODUCTS OF PROTEOLYTIC DIGESTION.
CC FURTHERMORE, THERE MAY BE A FUNCTIONAL SIGNAL SEQUENCE IN THE 30
CC KDA SPECIES WHICH IS UNCLEAVABLE IN THE SECRETION STEP.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- DISEASE: THE CONTINUOUS OVEREXPRESSION OF GAFS MAY LEAD TO

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CC MALIGANT CELL GROWTH CAUSED BY AN AUTOCRINE LOOP.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -1- DATABASE: NAME=R&D Systems' cytokine source book: FGF9;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=199".
CC -----
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CC -----
CC EMBL; D14838; BAA03572.1; -.
CC PIR; A4139378; CAC17692.1; -.
CC PDB; 1G82; 07-MAR-01.
CC MIN; 600921; -.
CC InterPro; IPR002209; HBGF_FGF.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF_1.
CC PRINTS; PR00262; IL1HBGF.
CC PRODOM; PD000831; HBGF_FGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Growth factor; Differentiation; Mitogen; Heparin-binding;
KW Glycoprotein; 3D-structure.
FT PROPEP 1 3 GLIA-ACTIVATING FACTOR.
FT CHAIN 4 208
FT CARBOHYD 79 79 N-LINKED (GLCNAC. .).
FT CONFLICT 24 26 VLP -> SLL (IN REF. 2).
FT CONFLICT 34 34 S -> A (IN REF. 2).
SQ SEQUENCE 208 AA; 23440 MW; F32A0E7106EF59C9 CRC64;

Query Match 69.3%; Score 774.5; DB 1; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.9e-65;
Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

QY 1 MAPLAEGVGLGLEGGLGQQVGSFHLPPAGERPPLIGERRSAAERSARG--GPGAAQL 57
Db 1 MAPLGEVGNVFGQDAV--PFGNVPVLPV--DSPVLLSDHLGQSE--AGGLPRGPAVTDL 54
QY 58 AHLHGILRRRLCYRTGFHLQILPDGSGVOGTRODHSFGILEFTISVAVGLVSTIRGVDSGL 117
Db 58 AHLHGILRRRLCYRTGFHLQILPDGSGVOGTRODHSFGILEFTISVAVGLVSTIRGVDSGL 114
QY 118 YLGMNDKGLYSGSEKLTSECIFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTTPR 177
Db 118 YLGMNDKGLYSGSEKLTSECIFRQFEENWNTYSSNIYKHGDTGRYFVALNKDGTTPR 174
QY 178 GARSKRHOKFTFLPRVDPVPELVKDLML 208
Db 178 GARSKRHOKFTFLPRVDPVPELVKDLML 205

RESULT 3
FGF9_MOUSE
ID FGF9_MOUSE STANDARD; PRT; 208 AA.
AC P54130;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).
GN FGF9 OR FGF-9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB;
RX MEDLINE=961139512; PubMed=8576175;

```

RA Santos-Ocampo S., Colvin J.S., Chelliah A.T., Ornitz D.M.:
 RT "Expression and biological activity of mouse fibroblast growth
 RT factor-9".
 RL J. Biol. Chem. 271:1726-1731(1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=95385801; PubMed=7656983;
 RA "Retinoic acid induces gene expression of fibroblast growth factor-9
 RT during induction of neuronal differentiation of mouse embryonal
 RT carcinoma P19 cells".
 RL FEBS Lett. 370:231-235(1995).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=96192599; PubMed=8619928;
 RA Hecht D., Zimmerman N., Bedford M., Avivi A., Yayon A.:
 RT "Identification of fibroblast growth factor 9 (FGF9) as a high
 RT affinity, heparin dependent ligand for FGF receptors 3 and 2 but not
 RT for FGF receptors 1 and 4".
 RL Growth Factors 12:223-233(1995).
 RN [4]
 RN SEQUENCE FROM N.A.
 RP STRAIN=129/SVJ;
 RA Colvin J.S., Feldman B., Nadeau J.H., Goldfarb M., Ornitz D.M.:
 RT "Genomic organization and embryonic expression of the mouse fibroblast
 RT growth factor 9 gene".
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
 CC DURING DEVELOPMENT, GLOSTIS DURING REPAIR AND REGENERATION OF
 CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
 CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
 CC -!- SUBCELLULAR LOCATION: Secreted
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 DR EMBL; U33535; AAC52529.1; -;
 DR EMBL; D38258; BAA07410.1; -;
 DR EMBL; S82023; AAB36429.1; -;
 DR EMBL; AF144626; AAD49222.1; -;
 DR EMBL; AF144624; AAD49222.1; JOINED.
 DR EMBL; AF144625; AAD49222.1; JOINED.
 DR HSSP; P05230; 2AEG.
 DR MGD; MGI:104723; Fgf9.
 DR InterPro; IPR002209; HBGF_FGF.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; HBGF_FGF; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 KW Growth factor; Differentiation; Mitogen; Heparin-binding;
 KW Glycoprotein.
 FT PROPEP 1 3 BY SIMILARITY.
 FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
 FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 208 AA; 23440 MW; E8DE1EEDFB70979E CRC64;
 Query Match 69.3%; Score 774.5; DB 1; Length 208;
 Best Local Similarity 70.6%; Pred. No. 1.9e-65;
 Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;
 QY 1 MAPLAEVGGFLGSLGQGVSHPLPAGRPPLGERSAERSARG---CPGAQL 57
 DB 1 MAPLAEVGGIFGQDAV--PFGNVPFLPV--DSPVLLMDHLGQSE--AGGLPRGPVATDL 54
 QY 58 AHLHGILRRQLYCRGTGFHLQILPDGVSQGTQDHSFLGILEFTSVAVGLSVRGVDSGL 117

DB 55 DHLKGLRRQLYCRGTGFHLQILPDGVSQGTQDHSFLGILEFTSVAVGLSVRGVDSGL 114
 QY 118 YLGMDKGLYSEKLTSECTFQFENNYSSNYKHGDTGRFYFVALNKDGTGPRD 177
 DB 115 YLGMDKGLYSEKLTSECTFQFENNYSSNYKHGDTGRFYFVALNKDGTGPRD 174
 QY 178 GARSKRHKQFTHLPVPDPVPDPVPELYKDL 208
 DB 175 GTRTKRHKQFTHLPVPDPVPDPVPELYKDL 205
 RESULT 4
 FGF9_RAT STANDARD; PRT; 208 AA.
 ID FGF9_RAT
 AC P36364;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
 DE (FGF-9) (HBGF-9).
 GN FGF9 OR FGF-9.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93309459; PubMed=8321227;
 RA Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
 RA Kurokawa T.;
 RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
 RT of the fibroblast growth factor family, which has a unique secretion
 RT property".
 RL Mol. Cell. Biol. 13:4251-4259(1993).
 CC -!- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
 CC DURING DEVELOPMENT, GLOSTIS DURING REPAIR AND REGENERATION OF
 CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
 CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: BRAIN AND KIDNEY.
 CC -!- PTM: N-GLYCOSYLATED.
 CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; D14839; BAA03573.1; -;
 DR HSSP; P05230; 2AEG.
 DR InterPro; IPR002209; HBGF_FGF.
 DR InterPro; IPR002348; IL1_HBGF.
 DR Pfam; PF00167; FGF; 1.
 DR PRINTS; PR00262; IL1HBGF.
 DR ProDom; PD000831; HBGF_FGF; 1.
 DR SMART; SM00442; FGF; 1.
 DR PROSITE; PS00247; HBGF_FGF; 1.
 KW Growth factor; Differentiation; Mitogen; Heparin-binding;
 KW Glycoprotein.
 FT PROPEP 1 3 BY SIMILARITY.
 FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
 FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 208 AA; 23413 MW; 4A3CB894DF643EB CRC64;
 Query Match 69.3%; Score 774.5; DB 1; Length 208;
 Best Local Similarity 70.6%; Pred. No. 1.9e-65;
 Matches 149; Conservative 23; Mismatches 30; Indels 9; Gaps 4;

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OY 1 MAPLAEVGGFLGGLGQQVSGSHFLPPACGERPPLLCGRSAAERSARG---GPGAAQL 57
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAPLGEVGSYFGVQDAV--PFGNVPLV--DSPVLLSDHLGQSE--AGGLPRGPVATDL 54
58 AHLHGILRRRLQCYCRTGFHLQILPDGSGVQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
55 DHLKGILRRRLQCYCRTGFHLGILEFIPNGTIQGTRODHSFLGILEFISVAVGLVSRGVDSGL 114
118 YLGMNDKELGYGSEKLTSECIFREOFENWYNTSSNIYKHGDTGRRYFVALNKDGTPRD 177
115 YLGMNEKELGYGSEKLTCECVFREOFENWYNTSSNIYKHVDTRGRRYFVALNKDGTPRE 174
OY 178 GARSKRHKQKTFHFLRPVDPDPVPELYKDIL 208
Db 175 GTRTKRHQKTFHFLRPVDPDPVPELYKDIL 205

RESULT 5
FGF9_XENLA
ID FGF9_XENLA STANDARD; PRT; 209 AA.
AC Q91875;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9) (XFGF-9).
GN FGF9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97006698; PubMed=8853991;
RA Song J., Slack J.M.W.;
RT "XFGF-9; a new fibroblast growth factor from Xenopus embryos.";
RL Dev. Dyn. 206:427-436(1996).
CC -!- FUNCTION: MAY HAVE A ROLE IN MUSCLE DEVELOPMENT AND NEURAL
CC DIFFERENTIATION, HAS NO SPECIFIC ROLE IN ANTEROPOSTERIOR
CC PATTERNING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MATERNAL TRANSCRIPT IS FOUND MAINLY IN THE
CC ANIMAL HEMISPHERE. ZYGOTIC TRANSCRIPT IS FOUND AROUND THE
CC BLASTOPORE AND IN THE LATE GASTRULA STAGE, IN THE DORSAL PART. IN
CC LATER STAGES IT IS FOUND ALONG THE DORSAL PART AND HEAD REGION.
CC -!- DEVELOPMENTAL STAGE: THE MATERNAL PROTEIN IS DETECTED UP TO THE
CC BLASTULA STAGE BUT DECLINES BY THE EARLY GLASTRULA. ZYGOTIC
CC EXPRESSION STARTS AT AROUND EARLY GASTRULA; THE LEVEL OF
CC EXPRESSION REACHED AT STAGE 15 PERSISTS DURING NEURULA AND TAILBUD
CC STAGES, AND IS FURTHER INCREASED DURING THE TADPOLE STAGES.
CC -!- PTM: KNOWN TO BE GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC
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CC
CC EMBL; U47622; AAC59936.1; -
CC HSP; P05230; 2AFG.
CC InterPro; IPR002209; HBGF_FGF.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; ILIHBGF.
CC ProDom; PD000831; HBGF_FGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Growth factor; Differentiation; Mitogen; Heparin-binding;
CC Glycoprotein.
CC KW
```

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FT PROPEP 1 3 BY SIMILARITY.
FT CHAIN 4 209 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 80 80 N-LINKED (GLCNAC...) (PROBABLE).
FT SEQUENCE 209 AA; 23662 MW; 26CBB229757FCBF CRC64;

Query Match 68.4%; Score 765; DB 1; Length 209;
Best Local Similarity 70.1%; Pred. No. 1.5e-64;
Matches 148; Conservative 16; Mismatches 39; Indels 8; Gaps 2;

OY 1 MAPLAEVGGFLGGLGQQVSGSHFLPPACGERPPLLCGRSAAERSARG---GPGAAQL 57
||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MAPLGEVGNVFG-----VQDAVSGNVPLQVDTPTVLLSDHSHSEAGGLPRGSVATDL 55
58 AHLHGILRRRLQCYCRTGFHLQILPDGSGVQGTRODHSFLGILEFISVAVGLVSRGVDSGL 117
56 EHLKGILRRRLQCYCRTGFHLGILEFIPNGTIQGTRODHSFLGILEFISVAVGLVSRGVDSGL 115
118 YLGMNDKELGYGSEKLTSECIFREOFENWYNTSSNIYKHGDTGRRYFVALNKDGTPRD 177
116 YLGMNEKELGYGSEKLTCECVFREOFENWYNTSSNIYKHADTGRYFVALNKDGTSRD 175
OY 178 GARSKRHKQKTFHFLRPVDPDPVPELYKDIL 208
Db 176 GTRTKRHQKTFHFLRPVDPDPVPELYKDIL 206

RESULT 6
FGF9_HUMAN
ID FGF9_HUMAN STANDARD; PRT; 207 AA.
AC Q43320;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-16 (FGF-16).
GN FGF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Heart;
RX MEDLINE=98139883; PubMed=9473496;
RA Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
RA Yamamoto S., Mikami T., Arakawa T., Itoh N.;
RT "Structure and expression of a novel member, FGF-16, on the fibroblast
RT growth factor family.";
RL Biochem. Biophys. Res. Commun. 243:148-152(1998).
CC -!- FUNCTION: INDUCES HEPATOCELLULAR PROLIFERATION. HAS NO BIOLOGICAL
CC EFFECT ON THE HEART (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted (by similarity).
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB009391; BAA24956.1; -
CC HSP; P05230; 2AFG.
CC MIM; 603724; -
CC InterPro; IPR002209; HBGF_FGF.
CC InterPro; IPR002348; IL1_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; ILIHBGF.
CC ProDom; PD000831; HBGF_FGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGF_FGF; 1.
CC Growth factor.
CC KW
```


[illegible]

Query Match	30.6%	Score	342.5	DB 1	Length	220			
Best Local Similarity	41.6%	Pred. No.	5.6e-25						
Matches	77	Conservative	29	Mismatches	56	Indels	23	Gaps	4
QY	26	LLP----	PAGERPPLGERRSAAERSARGGPGAAQIAHLHGLIRRRQRYCRTGFHQLIPL	81					
Db	11	LLPEPRVPAATASP-----	RAPDAGRGG----	VYELGGAPRRKKLYCATYHLQIHP	61				
QY	82	DGSVQCTRODHSLF	GILEFISAVGLVSTRGVDSGLYLCMNDKGBLYGSEKLTSCSIFRE	141					
Db	62	GKINGTLEKNSVFS	LEITAVDVGIVAIKGLFSGRYLAMNKRGLYASENYNTCEFPVE	121					
QY	142	QFENNYNTYSSN	YIKHGDG-----	RRYFVALNKDGTTPRDGARSKKRQFETHFL	191				
Db	122	KIHELGYNTYASRLY	TVTVPSCGASTKKKSAERLWYVSVNGKGRPRGFKTRRTQKSSLFL	181					
QY	192	PRPVD	196						
Db	182	PRVLD	186						

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RESULT 9
FGF5_RAT
ID FGF5_RAT STANDARD; PRT; 266 AA.
DT P48807; Q63402;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE FIBROblast growth factor-5 precursor (FGF-5) (HBGF-5).
GN FGF5 OR FGF-5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
STRAIN=WISTAR;
RC MEDLINE=96201703; PubMed=8611621;
RX Hattori Y., Yamasaki M., Itoh N.;
RA "The rat FGF-5 mRNA variant generated by alternative splicing encodes
RT a novel truncated form of FGF-5.";
RL Biochem. Biophys. Acta 1306:31-33(1996).
CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM/FGF-5S; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -|- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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-----
CC EMBL; D64085; BAA10966.1; -.
CC DR EMBL; D64086; BAA10967.1; -.
CC DR HSSP; P09038; 1BFG.
CC DR InterPro; IPR002209; HBGF_FGF.
CC DR InterPro; IPR002348; IIL_HBGF.
CC DR Pfam; PF00167; FGF; 1.
CC DR PRINTS; PR00262; ILLHBGF.
CC DR ProDom; PD000831; HBGF_FGF; 1.
CC DR SMART; SM00442; FGF; 1.
CC DR PROSITE; PS00247; HBGF_FGF; 1.
KW Proto-oncogene; Growth factor; Mitogen; Signal; Alternative splicing.
FT SIGNAL 1 17
FT CHAIN 18 266
FT DOMAIN 54 59
FT CARBOHYD 108 108
FT VARSPPLIC 118 121
FT VARSPPLIC 122 266
FT SEQUENCE 266 AA; 29264 MW; 95E0A0CA7C0A200C CRC64;

```



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FGF3_HUMAN
ID FGF3_HUMAN STANDARD; PRT; 239 AA.
AC P11487;
DT 01-OCT-1989 (Rel. 12, Created)
DE 01-OCT-1989 (Rel. 12, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
DE (FGF-3) (HBGF-3).
DE GN FGF3 OR FGF-3 OR INT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=86247582; PubMed=3013624;
RA Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT "Sequence, topography and protein coding potential of mouse int-2: a
RT putative oncogene activated by mouse mammary tumour virus.";
RL EMBO J. 5:919-924 (1986).
RN [2]
RX SEQUENCE OF 1-73 FROM N.A.
RX MEDLINE=88296404; PubMed=2841106;
RA Smith R., Peters G., Dickson C.;
RT "Multiple RNAs expressed from the int-2 gene in mouse embryonal
RT carcinoma cell lines encode a protein with homology to fibroblast
RT growth factors."
RL EMBO J. 7:1013-1022 (1988).
RN [3]
RX CHARACTERIZATION.
RX MEDLINE=91193291; PubMed=1964688;
RA Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D.,
RA Walther W., Fuller-Pace F., Kiefer P., Peters G.;
RT "Characterization of int-2: a member of the fibroblast growth factor
RT family.";
RL J. Cell Sci. Suppl. 13:87-96 (1990).
CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC -1- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC
CC EMBL: Y00848; CAA68767.1; -.
DR PIR: A23930; TVMST2.
DR HSP: P09038; IBFG.
DR MGI: 95517; Fgf3.
DR InterPro: IPR002209; HBGF_FGF.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HBGF_FGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
KW Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 245 INT-2 PROTO-ONCOGENE PROTEIN.
FT CARBOHYD 65 65 N-LINKED (GLCNAC...).
SQ SEQUENCE 245 AA; 27214 MW; 70D94FD6A7837C79 CRC64;
Query Match 28.5%; Score 319; DB 1; Length 239;
Best Local Similarity 41.1%; Pred. No. 9.8e-23;
Matches 78; Conservative 29; Mismatches 61; Indels 22; Gaps 6;
QY 28 PPAGERPPLGERRSAAERSARGGGAQAHLHGLRRRLQYCRGTGHLQILPDGSGVQG 87
Dd 17 PAAGPGCARL-----GGRGVV-YEHLGGAPRRKLYCATKYHLQLHPGSRVNG 66
QY 88 TRQDHSFLGILFISVANGLYSIRVDSGLYGLNMDKGYLSEKLTSECFRQEEFNW 147
Dd 67 S-LENSAYSILEITAVEGVIAIRGLFSGRYLA MKRGRLYASEHVSACEFVERIHEL 125
QY 148 YNTYSSNIY-----KHGDTGRRYFVALNKDGPFGCARSKRHKFTFLPRPVP 197
Dd 126 YNTYASRLYRTVSTPGARRQPSAERLWVSVNGKGRPRRGFKTRRTQKSSFLPRVLD 184
QY 198 ERVPELYKDL 207
Dd 185 HRDHVMYRQL 194
RESULT 15
FGF3_MOUSE
ID FGF3_MOUSE STANDARD; PRT; 245 AA.
AC P05524;
DT 01-NOV-1988 (Rel. 09, Created)
DE 01-NOV-1988 (Rel. 09, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE INT-2 proto-oncogene protein precursor (Fibroblast growth factor-3)
DE (FGF-3) (HBGF-3).
DE GN FGF3 OR FGF-3 OR INT-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
OX [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=86247582; PubMed=3013624;
RA Moore R., Casey G., Brookes S., Dixon M., Peters G., Dickson C.;
RT "Sequence, topography and protein coding potential of mouse int-2: a
RT putative oncogene activated by mouse mammary tumour virus.";
RL EMBO J. 5:919-924 (1986).
RN [2]
RX SEQUENCE OF 1-73 FROM N.A.
RX MEDLINE=88296404; PubMed=2841106;
RA Smith R., Peters G., Dickson C.;
RT "Multiple RNAs expressed from the int-2 gene in mouse embryonal
RT carcinoma cell lines encode a protein with homology to fibroblast
RT growth factors."
RL EMBO J. 7:1013-1022 (1988).
RN [3]
RX CHARACTERIZATION.
RX MEDLINE=91193291; PubMed=1964688;
RA Dickson C., Acland P., Smith R., Dixon M., Deed R., McAllan D.,
RA Walther W., Fuller-Pace F., Kiefer P., Peters G.;
RT "Characterization of int-2: a member of the fibroblast growth factor
RT family.";
RL J. Cell Sci. Suppl. 13:87-96 (1990).
CC -1- FUNCTION: COULD BE INVOLVED IN EAR DEVELOPMENT.
CC -1- INDUCTION: BY INTEGRATION OF MOUSE MAMMARY TUMOR VIRUS.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC
CC EMBL: Y00848; CAA68767.1; -.
DR PIR: A23930; TVMST2.
DR HSP: P09038; IBFG.
DR MGI: 95517; Fgf3.
DR InterPro: IPR002209; HBGF_FGF.
DR InterPro: IPR002348; IL1_HBGF.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR ProDom: PD000831; HBGF_FGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
KW Proto-oncogene; Growth factor; Mitogen; Signal; Glycoprotein.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 239 INT-2 PROTO-ONCOGENE PROTEIN.
FT CARBOHYD 65 65 N-LINKED (GLCNAC...).
SQ SEQUENCE 239 AA; 26886 MW; 8DBEF17D2B2E3C63 CRC64;
Query Match 28.5%; Score 319; DB 1; Length 239;
Best Local Similarity 41.1%; Pred. No. 9.8e-23;
Matches 78; Conservative 29; Mismatches 61; Indels 22; Gaps 6;
QY 28 PPAGERPPLGERRSAAERSARGGGAQAHLHGLRRRLQYCRGTGHLQILPDGSGVQG 87
Dd 17 PAAGPGCARL-----GGRGVV-YEHLGGAPRRKLYCATKYHLQLHPGSRVNG 66
QY 88 TRQDHSFLGILFISVANGLYSIRVDSGLYGLNMDKGYLSEKLTSECFRQEEFNW 147
Dd 67 S-LENSAYSILEITAVEGVIAIRGLFSGRYLA MKRGRLYASEHVSACEFVERIHEL 125
QY 148 YNTYSSNIY-----KHGDTGRRYFVALNKDGPFGCARSKRHKFTFLPRPVP 197
Dd 126 YNTYASRLYRTVSTPGARRQPSAERLWVSVNGKGRPRRGFKTRRTQKSSFLPRVLD 184
QY 198 ERVPELYKDL 207
Dd 185 HRDHVMYRQL 194
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Db 84 GVAIKGLESGRYLANKRGLYASDHYNACEFEVERIHELGYNTYASRLYRTGSSGPGA 143

Qy 163 -----RRYFVALNKDGTPRDGCARSKRHQKFTHELPR 193

Db 144 QROPQAORPWYVSVNGKGRPRGFKTRRTQKSSFLPR 181

Search completed: October 21, 2002, 16:14:33
Job time : 13 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model .
Run on: October 21, 2002, 16:10:50 ; Search time 27 Seconds
(without alignments)
1351.923 Million cell updates/sec

Title: US-09-817-814-2
perfect score: 1118
Sequence: 1 MAPLAEVGFGGLEGIGQQ.....PRPVDPREVPELYKPLLMT 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

00000000007 .11361917 has aa unmuttynv

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:★

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1079	96.1	212	11	Q9EST9	Q9est9 rattus norv
2	1064	95.6	212	11	Q9ESL9	Q9esl9 mus musculus
3	80.9	80.9	208	13	Q9PVL1	Q9pvl1 xenopus lae
4	774.5	69.3	208	6	Q95LI2	Q95li2 sus scrofa
5	707.5	63.3	207	11	Q9ERQ5	Q9erq5 mus musculus
6	700.5	62.7	207	11	Q9ESL8	Q9esl8 mus musculus
7	316.5	28.3	253	13	Q9IA15	Q9iai5 gallus gall
8	316.5	28.3	237	13	Q9IA16	Q9iai6 gallus gall
9	312	27.9	252	11	Q89096	Q89096 rattus norv
10	308	27.5	208	6	Q95K97	Q95k97 macaca fasc
11	304.5	27.2	212	13	Q42407	Q42407 gallus gall
12	304	27.2	302	11	Q9CSX5	Q9csx5 mus musculus
13	303.5	27.1	245	13	Q9W6A2	Q9w6a2 gallus gall
14	303	27.1	199	13	Q9IA13	Q9iai3 gallus gall
15	300	26.8	200	4	Q96P59	Q96p59 homo sapien
16	299	26.7	192	11	Q9ERW3	Q9erw3 rattus norv

17	295.5	26.4	213	6	Q9N1B9
18	291	26.0	181	11	Q924B4
19	289	25.8	243	13	Q9W6A1
20	288	25.8	181	13	Q9TA17
21	279	25.0	127	4	Q99517
22	278	25.0	191	13	Q9DFC9
23	278	24.9	425	5	Q76831
24	277	24.8	134	13	Q90XQ3
25	272.5	24.4	206	13	Q9YGD8
26	268	24.0	186	6	Q95L47
27	266	23.8	196	13	Q9YH31
28	262	23.4	185	11	Q9ERN5
29	260.5	23.3	124	13	Q90XQ5
30	260	23.3	112	13	Q90XP9
31	241	21.6	111	13	Q90Y71
32	238.5	21.3	129	4	Q60371
33	234.5	21.0	111	13	Q90XQ1
34	214.5	19.2	196	4	F78443
35	213	19.1	770	5	P91672
36	213	19.1	770	5	Q9VDR9
37	210	18.8	155	13	Q90Y92
38	204.5	18.3	106	6	Q9N1S8
39	202.5	18.1	130	6	Q77767
40	194.5	17.4	125	13	Q98YD8
41	193.5	17.3	97	4	Q9NSJ0
42	193	17.3	153	11	Q925A3
43	187	16.7	170	11	Q60487
44	176.5	15.8	101	13	P79706
45	176.5	15.8	210	13	Q57341

ALIGNMENTS

RESULT 1

Q9EST9	PRELIMINARY;	PRT;	212 AA.
AC	Q9EST9;		
AD	Q9EST9;		
AT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	FGF-20.		
GN	FGF-20.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxId=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=ADULT BRAIN;		
FX	MEDLINE=20490008; PubMed=11032730;		
RA	Ohmachi S., Watanabe Y., Mikami T., Kusu N., Ibi T., Akaike A.,		
RA	Itoh N.		
RT	"FGF-20, a novel neurotrophic factor, preferentially expressed in the		
RL	substantia nigra pars compacta of rat brain."		
RL	Biochem. Biophys. Res. Commun. 277:355-360(2000).		

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Query Match      96.1%; Score 1074; DB 11; Length 212;
Best Local Similarity 95.3%; pred. No. 4e-98;
Matches 201; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      1 MAPLEVGFLGEGLEGQGVGSHFLPPLGAGERPPLIGRRSAAERSGGPGAAQLAHL 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 1 MAPLTVGAFGLGGLEGQQVGSFHLPPAGERPPLLGERGALRGARGGSGVELAHL 60
Qy 61 HGILRRQLYCRGTGFHLQILPDGVSQGTQDHSLSFGILFISVAVGLVSRGVDSGLYL 120
Db 61 HGILRRQLYCRGTGFHLQILPDGVSQGTQDHSLSFGILFISVAVGLVSRGVDSGLYL 120
Qy 121 MNDKGYLGSSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Db 121 MNGKGYLGSSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Qy 181 SKRHQKFTHLPRVDPERPVELYKDLLMYT 211
Db 181 SKRHQKFTHLPRVDPERPVELYKDLLMYT 211
RESULT 2
Q9ESL9
ID Q9ESL9 PRELIMINARY; PRT; 212 AA.
AC Q9ESL9;
DT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DE 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 20.
GN FGF20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Mus musculus mRNA for FGF-20 (FGF20).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049218; BAB16406.1; -.
DR HSSP; P31371; IG82.
DR MGB; MGI:1891346; Fgf20.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; ILI_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;

Query Match 95.6%; Score 1069; DB 11; Length 212;
Best Local Similarity 94.8%; Pred. No. 1.2e-97;
Matches 200; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MAPLAEVGGFLGGLEGQQVGSFHLPPAGERPPLLGERSAERSARGGPGAAQLAHL 60
Db 1 MAPLTVGAFGLGGLEGQQVGSFHLPPAGERPPLLGERGALRGARGGSGVELAHL 60
Qy 61 HGILRRQLYCRGTGFHLQILPDGVSQGTQDHSLSFGILFISVAVGLVSRGVDSGLYL 120
Db 61 HGILRRQLYCRGTGFHLQILPDGVSQGTQDHSLSFGILFISVAVGLVSRGVDSGLYL 120
Qy 121 MNDKGYLGSSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Db 121 MNDKGYLGSSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Qy 181 SKRHQKFTHLPRVDPERPVELYKDLLMYT 211
Db 181 SKRHQKFTHLPRVDPERPVELYKDLLMYT 211
RESULT 3
Q9PVY1
ID Q9PVY1 PRELIMINARY; PRT; 208 AA.
AC Q9PVY1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
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DE XFGF-20.
GN XFGF-20.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93373151; PubMed=10441498;
RA Kopa C., Adati N., Nakata K., Mikoshiba K., Furuhashi Y., Sato S.,
RA Tei H., Sakaki Y., Nakokawa T., Shikawa K., Yokoyama K.K.;
RT "Characterization of a novel member of the FGF family, XFGF-20, in
RT Xenopus laevis.";
RL Biochem. Biophys. Res. Commun. 261:756-765(1999).
DR EMBL; AB012615; BAA83474.1; -.
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; ILI_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHGFG.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
SQ SEQUENCE 208 AA; 23438 MW; 268881D36E757D4D CRC64;

Query Match 80.9%; Score 904.5; DB 13; Length 208;
Best Local Similarity 80.6%; Pred. No. 2.2e-81;
Matches 170; Conservative 19; Mismatches 19; Indels 3; Gaps 2;

Qy 1 MAPLAEVGGFLGGLEGQQVGSFHLPPAGERPPLLGERSAERSARGGPGAAQLAHL 60
Db 1 MAPLADVGTFLGGYDALG-QVGSFHLPPAKDSPLLFNDPLAQSERLSRSAP--SDLSHL 57
Qy 61 HGILRRQLYCRGTGFHLQILPDGVSQGTQDHSLSFGILFISVAVGLVSRGVDSGLYL 120
Db 58 QGILRRQLYCRGTGFHLQILPDGVSQGTQDHSLSFGILFISVAVGLVSRGVDSGLYL 117
Qy 121 MNDKGYLGSSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTPRDGR 180
Db 118 MNDKGYLGSSEKLTSECIFREQFEENWNTYSSNIYKHGDSGRYFVALNKDGTPRDGT 177
Qy 181 SKRHQKFTHLPRVDPERPVELYKDLLMYT 211
Db 178 AKRHQKFTHLPRVDPERPVELYKDLGYS 208

RESULT 4
Q95L12
ID Q95L12 PRELIMINARY; PRT; 208 AA.
AC Q95L12;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 9.
GN FGF9.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Paradis V., Silversides D.W.;
RT "Sus scrofa fgf9 cDNA.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY033825; AAK61609.2; -.
SQ SEQUENCE 208 AA; 23454 MW; 05FD0E2048CC5E5 CRC64;

Query Match 69.3%; Score 774.5; DB 6; Length 208;
Best Local Similarity 70.6%; Pred. No. 1.5e-68;
Matches 149; Conservative 24; Mismatches 29; Indels 9; Gaps 4;

Qy 1 MAPLAEVGGFLGGLEGQQVGSFHLPPAGERPPLLGERSAERSARG--GFGAAQL 57
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Db 1 MAPLGEVGNFYGVQDAV--PFCNVPVLPV--DSPVLLSDHLSQSE--AGGLPRGPVATDL 54
QY 58 AHLHGILRRQLCYRTGTHLQILPDGSGVQGTQDHSFLGFIIEFISVAVGLVIRGVDGSL 117
Db 55 DHLKGLLRRLQCYRTGTHLQILPDGSGVQGTQDHSFLGFIIEFISVAVGLVIRGVDGSL 114
QY 118 YLGMNDKGLYSGKLTSCIPREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGTPRD 177
Db 115 YLGMNEKGLYSGKLTSCIPREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGTPRE 174
QY 178 GASKRHQKFTHELPRVDPVPRVPELYKDLL 208
Db 175 GTRTKRHQKFTHELPRVDPVPRVPELYKDLL 205

RESULT 5
Q9ERQ5 PRELIMINARY; PRT; 207 AA.
ID Q9ERQ5
AC Q9ERQ5;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FGF-16 PROTEIN.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sontag D.P., Cattini P.A.;
RT Cloning and biological function of FGF-16 in the heart.;
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292104; AAG29501.1; -.
DR HSSP; P31371; IG82.
DR MGD; MGI:1931627; Fgf16.
DR InterPro; IPR002209; HBG_FGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILI_HBGF.
DR ProDom; PD000831; HBG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBG_FGF; 1.
SQ SEQUENCE 207 AA; 23739 MW; E28004DED598A2C6 CRC64;

Query Match 63.3%; Score 707.5; DB 11; Length 207;
Best Local Similarity 63.2%; Pred. No. 6.3e-62;
Matches 134; Conservative 27; Mismatches 60; Indels 11; Gaps 4;

QY 4 LAEVGGFLGG---LEGLGQQVGSFHLPPAGERPPLLGERRSAAE-RSARGGPGAAQLA 58
Db 1 MAEVGGVFASLDWDLQGFSSSLGN---VPLADSPGFLNERLQIEGKLRGSP--TDFA 54
QY 59 HLHGILRRQLCYRTGTHLQILPDGSGVQGTQDHSFLGFIIEFISVAVGLVIRGVDGSL 118
Db 55 HLKGLLRRLQCYRTGTHLQILPDGSGVQGTQDHSFLGFIIEFISVAVGLVIRGVDGSL 114
QY 119 LGMNDKGLYSGKLTSCIPREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGTPRD 178
Db 115 LGMNERGELYGSKLTRECVCFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGTPRD 174
QY 179 ARSKRHQKFTHELPRVDPVPRVPELYKDLLMY 210
Db 175 YRTKRHKQKFTHELPRVDPVPRVPELYKDLLMY 206

RESULT 6
Q9ESL8 PRELIMINARY; PRT; 207 AA.
ID Q9ESL8
AC Q9ESL8;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FGF-4.
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20112823; PubMed=10644718;
RT Munoof-Sanjuan I., Smallwood P.M., Nathans J.;
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.";
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199606; AAF31393.1; -.
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBG_FGF.
DR Pfam; PF00167; FGF; 1.

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DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 16.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Mus musculus mRNA for FGF-16 (FGF16).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049219; BAB16405.1; -.
DR HSSP; P31371; IG82.
DR MGD; MGI:1931627; Fgf16.
DR InterPro; IPR002209; HBG_FGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILI_HBGF.
DR ProDom; PD000831; HBG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBG_FGF; 1.
SQ SEQUENCE 207 AA; 23751 MW; 68BD03EBDAALD84E CRC64;

Query Match 62.7%; Score 700.5; DB 11; Length 207;
Best Local Similarity 62.7%; Pred. No. 3.1e-61;
Matches 133; Conservative 27; Mismatches 41; Indels 11; Gaps 4;

QY 4 LAEVGGFLGG---GLCQQVGSFHLPPAGERPPLLGERRSAAE-RSARGGPGAAQLA 58
Db 1 MAEVGGVFASLDWDLHGFSSSLGN---VPLADSPGFLNERLQIEGKLRGSP--TDFA 54
QY 59 HLHGILRRQLCYRTGTHLQILPDGSGVQGTQDHSFLGFIIEFISVAVGLVIRGVDGSL 118
Db 55 HLKGLLRRLQCYRTGTHLQILPDGSGVQGTQDHSFLGFIIEFISVAVGLVIRGVDGSL 114
QY 119 LGMNDKGLYSGKLTSCIPREQFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGTPRD 178
Db 115 LGMNERGELYGSKLTRECVCFEENWYNTYSSNIYKHGDTGRRYFVALNKDGTGTPRD 174
QY 179 ARSKRHQKFTHELPRVDPVPRVPELYKDLLMY 210
Db 175 YRTKRHKQKFTHELPRVDPVPRVPELYKDLLMY 206

RESULT 7
Q9IAI5 PRELIMINARY; PRT; 253 AA.
ID Q9IAI5
AC Q9IAI5;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 4 ISOFORM 1B.
GN FGF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20112823; PubMed=10644718;
RT Munoof-Sanjuan I., Smallwood P.M., Nathans J.;
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.";
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL; AF199606; AAF31393.1; -.
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBG_FGF.
DR Pfam; PF00167; FGF; 1.

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DR PRINTS: PR00262; IL1HBGF.
DR PRODOM: PD000831; HBGF_FGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
SQ SEQUENCE 253 AA; 28640 MW; 5AEFD9F9D6E74305 CRC64;

Query Match 28.3%; Score 316.5; DB 13; Length 253;
Best Local Similarity 38.4%; Pred. No. 3.6e-23;
Matches 71; Conservative 34; Mismatches 61; Indels 19; Gaps 4;

QY 22 GSHFLLPAGERPPLGERRSAARSARGPGAQAHLHLGILRRRLQYCRTFGHLQILP 81
DB 50 GSHMLQCLCG-----KSLKKNKNTDP-----QLKGIVTR--LYCRQGYLQMH 92

QY 82 DGSVOGTRODHSFLGILFISVAVGLVIRGVDGSLYLGMDKGLYSEKLTSECFIRE 141
DB 93 DGSGLGTDKDDSSNSLFLNLPVGLRVVAIOGVKTLGLYIALNNEGFLYTSFLTP 152

QY 142 QFEENWYNTSSNIYKHGDTGRYFVALNKDGTPRDGARSRHOKFTHFLPRVPDPE--R 199
DB 153 SVFENYVIYSSMLYRQESGRAWFLGLNKGQVMKGNRVKTKPAAHFLPKPLEVAMY 212

QY 200 VPELY 204
DB 213 EPSLH 217

RESULT 8
Q9IAI6 PRELIMINARY; PRT; 237 AA.
AC Q9IAI6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 4 ISOFORM 1A
DE (FRAGMENT).
GN FGF-4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112823; PubMed=10644718.
RA Munoz-Sanjuan I., Smallwood P.M., Nathans J.;
RT "Isoform Diversity among Fibroblast Growth Factor Homologous Factors
RT Is Generated by Alternative Promoter Usage and Differential
RT Splicing.";
RL J. Biol. Chem. 275:2589-2597(2000).
DR EMBL: AF199605; AAF31392.1; -.
DR HSSP: P31371; IG82.
DR InterPro: IPR002209; HBGF_FGF.
DR SMART: SM00442; FGF; 1.
DR PRODOM: PD000831; HBGF_FGF; 1.
DR PRINTS: PR00262; IL1HBGF.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
FT NON_TER 1
SQ SEQUENCE 237 AA; 26816 MW; F13076736548BB22 CRC64;

Query Match 28.3%; Score 316; DB 13; Length 237;
Best Local Similarity 43.5%; Pred. No. 3.7e-23;
Matches 64; Conservative 31; Mismatches 48; Indels 4; Gaps 2;

QY 60 LHGILRRRLQYCRTFGHLQILPDGSGVGTQRDHSFLGILEFISVAVGLVIRGVD 119
DB 57 LKGIVTR--LYCRQGYLQMHDPGSLDGTDDSSNSTLFLNLPVGLRVVAIOGVK 114

QY 120 GMNDKGLYSEKLTSCIFRQEFENWYNTSSNIYKHGDTGRYFVALNKDGT 179
DB 115 ALNNEGFLYTSFLTPCKFKESVFENYVIYSSMLYRQESGRAWFLGLNKGQVM 174
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QY 180 RSKRHQKFTHELPRPVDPE--RVPELY 204
DB 175 RVKTKPAAHFLPKPLEVAMYPELSLH 201

RESULT 9
O89096 PRELIMINARY; PRT; 252 AA.
AC O89096;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FGF-4B.
GN FGF14.
OS Rattus norvegicus (Rat), and
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116, 10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE=98267141; PubMed=9602045;
RA Yamamoto S., Mikami T., Ohbayashi N., Ohta M., Itoh N.;
RT "Structure and expression of a novel isoform of mouse FGF homologous
RT factor (FGF)-4.";
RL Biochim. Biophys. Acta 1398:38-41(1998).
DR EMBL: AB008908; BAA31544.1; -.
DR HSSP: P31371; IG82.
DR MGD: MGI:109189; Fgf14.
DR InterPro: IPR002209; HBGF_FGF.
DR Pfam: PF00167; FGF; 1.
DR PRODOM: PD000831; HBGF_FGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGF_FGF; 1.
SQ SEQUENCE 252 AA; 28364 MW; 281781EEBA63AB44 CRC64;

Query Match 27.9%; Score 312; DB 11; Length 252;
Best Local Similarity 42.9%; Pred. No. 9.9e-23;
Matches 63; Conservative 31; Mismatches 49; Indels 4; Gaps 2;

QY 60 LHGILRRRLQYCRTFGHLQILPDGSGVGTQRDHSFLGILEFISVAVGLVIRGVD 119
DB 73 LKGIVTR--LYCRQGYLQMHDPGSLDGTDDSSNSTLFLNLPVGLRVVAIOGVK 130

QY 120 GMNDKGLYSEKLTSCIFRQEFENWYNTSSNIYKHGDTGRYFVALNKDGT 179
DB 131 AMNGEGYLYPSELTPCKFKESVFENYVIYSSMLYRQESGRAWFLGLNKGQVM 190

QY 180 RSKRHQKFTHELPRPVDPE--RVPELY 204
DB 191 RVKTKPAAHFLPKPLEVAMYPELSLH 217

RESULT 10
Q95K97 PRELIMINARY; PRT; 208 AA.
AC Q95K97;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL 23.5 KDA PROTEIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MEDULLA OBLOGATA;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
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RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RL libraries";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB063051; BAB60779.1; -.
KW Hypothetical protein.
SQ SEQUENCE 208 AA; 23466 MW; 0766A787609B3661 CRC64;

Query Match 27.5%; Score 308; DB 6; Length 208;
Best Local Similarity 35.9%; Pred. No. 1.9e-22;
Matches 65; Conservative 37; Mismatches 67; Indels 12; Gaps 2;

QY 15 EQLGQGVSHFLPPAGSRPPLGERRSAAERSARGPGGAQLAHLHGILRRRLQYCTG 74
   : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 38 QALGQDMVS-----PETTSSSSSFSSPSSAGHRVSYNHLQGDVYRWKLFSTFK 87
   : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 75 FHLQLPDGSVQGTRODHSFGILEFTSVAGLVIRGVDSGLYGLMNDKGELVGSSEKLT 134
   : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 88 YFLKTRKNGVSGTKKNCPSILEITSVEIGVVAVKAINSYNYLAMNKKGLYGSKEFN 147
   : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 135 ECIFRQFENWNTYSSNIYKHGDTGRRYFVALNKDGTGPRDGAQRKHQKTHFLPRP 194
   : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 148 NDCKLKERIEENGNTYASFWNQH--NGRQMYVALNGKGAAPRGQKTRKNTSAHFLLPMV 205
   : ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 195 V 195
Db 206 V 206

RESULT 11
042407 PRELIMINARY; PRT; 212 AA.
AC 042407;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 10.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=97330690; PubMed=9187149;
RA Onuchi H., Nakagawa T., Yamamoto A., Araga A., Ohta T., Ishimaru Y.,
RA Yoshio H., Kuwana T., Nohno T., Yamasaki M., Itoh N., Noji S.;
RT "The mesenchymal factor, FGF10, initiates and maintains the outgrowth
RT of the chick limb bud through interaction with FGF8, an apical
RT ectodermal factor";
RL Development 124:2235-2244(1997).
DR EMBL; D86333; BAA24945.1; -.
DR HSSP; P31371; 1G82.
DR InterPro; IPR002209; HBGF_FGF.
DR Pfam; PF00167; FGF; 1.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR SWART; SM00442; FGF; 1.
SQ SEQUENCE 212 AA; 23631 MW; AB4C0B32C72A0D90 CRC64;

Query Match 27.2%; Score 304.5; DB 13; Length 212;
Best Local Similarity 37.2%; Pred. No. 4.3e-22;
Matches 67; Conservative 35; Mismatches 67; Indels 11; Gaps 3;

QY 21 VGSFLLPPAGERPPLGERRSAAERSARGPGGA-----QLAHLHGILRRRLQYCTG 75
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Db 37 LGQDMLSPATNS-----SSSSSSSFSSPSSAGHRVSYNHLQGDVYRWKLFSTFK 92
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 76 HLOILPDGSVQGTRODHSFGILEFTSVAGLVIRGVDSGLYGLMNDKGELVGSSEKLT 135
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Db 93 FLKTRKNGVSGTKKNCPSILEITSVEIGVVAVKAINSYNYLAMNKKGLYGSKEFN 152
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QY 136 ECIFRQFENWNTYSSNIYKHGDTGRRYFVALNKDGTGPRDGAQRKHQKTHFLPRPV 195
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Db 153 DCKLKERIEENGNTYASLNWKH--NGRQMFVALNGRGATKRGQKTRKNTSAHFLLPMV 210
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RESULT 12
Q9CSX5 PRELIMINARY; PRT; 302 AA.
AC Q9CSX5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 12 (FRAGMENT).
GN FGF12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1;
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK011712; BAB27794.1; -.
DR HSSP; P31371; 1G82.
DR MGD; MGI:109183; Fgf12.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR NON_TER 1.
FT NON_TER 1.
SQ SEQUENCE 302 AA; 32720 MW; 22CC34A01B446D5C CRC64;

Query Match 27.2%; Score 304; DB 11; Length 302;
Best Local Similarity 32.7%; Pred. No. 7.9e-22;
Matches 69; Conservative 39; Mismatches 65; Indels 38; Gaps 4;

QY 29 PAGERPPLGERRSAAERSARGPGGAOLA----- 58
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Db 68 PGAPRRPSLGRSSGGGRGA--GRPCASLSMKILALSLLKGVHMLQCLGRSLRSSDPS 125
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 59 --HLHGILRRRLQYCTGFIHQILPDGSVQGTRODHSFGILEFTSVAGLVIRGVDSG 116
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 126 EPQLAGIVTR--LFSQOQGYFLQHPDGDIDGTDKDNSYTFLENLPVGRVVAIOGVKAS 183
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 117 LYLGMNDKGELVGSSEKLTSECFRQFENWNTYSSNIYKHGDTGRRYFVALNKDGTGPR 176
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 184 LYVANNGEGLYSSDVFTPECKFKESVPENYVYVYSSLYRQESGRAWFLGLNKEGQIM 243
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 177 DGARSKRKHQKTHFLPRPVD--PERVPELYK 205
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 244 KGNRVKTKPSSHFPKPIEVCMTREPSLHE 274
   : | | | : | : | : | : | : | : | : | : | : | : | : | : | : |

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Db 148 NDCKLXRIEENGYNFYASFNNQH--NGRQMYVALNGKGAPRGOKTRKNTSAHFLLPMV 205

OY 195 V 195

Db 206 V 206

Search completed: October 21, 2002, 16:15:09
Job time : 30 secs

GenCore version 5.1.1.3

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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:15:16 ; Search time 31 seconds
(without alignments)
756.018 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 211

Sequence: 1 MAPLAEVGGFLGLELGGQ.....PRPVDPERVELYKDLLMYT 211

Scoring table: OLIGO

Gapop 60.0 , Capext 60.0

Searched: 747574 seqs, 11107396 residues

Word size: 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database: A_Geneseq_032802.*

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	211	AA18635	Amino acid sequenc
2	211	100.0	211	AAU09931	Human fibroblast g
3	211	100.0	211	AAU09931	Human fibroblast g
4	211	100.0	211	AAU02081	Human fibroblast g
5	211	100.0	211	AAU02081	Human fibroblast g
6	85	40.3	212	AAU02081	Rat fibroblast gro
7	19	9.0	142	AAU02080	Glia activating fa
8	19	9.0	159	AAU02080	Glia activating fa
9	19	9.0	160	AAU02080	Glia activating fa
10	19	9.0	175	AAU02080	Glia activating fa
11	19	9.0	176	AAU02080	Glia activating fa

12	19	9.0	177	13	AAU02080	Glia activating fa
13	19	9.0	178	13	AAU02080	Glia activating fa
14	19	9.0	205	13	AAU02080	Glia activating fa
15	19	9.0	205	15	AAU02080	Glia activating fa
16	19	9.0	206	13	AAU02080	Glia activating fa
17	19	9.0	206	13	AAU02080	Glia activating fa
18	19	9.0	206	15	AAU02080	Glia activating fa
19	19	9.0	207	15	AAU02080	Glia activating fa
20	19	9.0	208	13	AAU02080	Glia activating fa
21	19	9.0	208	13	AAU02080	Glia activating fa
22	19	9.0	208	15	AAU02080	Glia activating fa
23	19	9.0	208	15	AAU02080	Glia activating fa
24	19	9.0	208	16	AAU02080	Glia activating fa
25	19	9.0	208	16	AAU02080	Glia activating fa
26	19	9.0	208	18	AAU02080	Glia activating fa
27	19	9.0	208	19	AAU02080	Glia activating fa
28	19	9.0	208	21	AAU02080	Glia activating fa
29	19	9.0	208	21	AAU02080	Glia activating fa
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31	19	9.0	208	21	AAU02080	Glia activating fa
32	19	9.0	208	22	AAU02080	Glia activating fa
33	19	9.0	208	22	AAU02080	Glia activating fa
34	19	9.0	208	22	AAU02080	Glia activating fa
35	19	9.0	208	22	AAU02080	Glia activating fa
36	19	9.0	208	22	AAU02080	Glia activating fa
37	19	9.0	208	22	AAU02080	Glia activating fa
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49	16	7.6	207	22	AAU02080	Glia activating fa
50	16	7.6	207	22	AAU02080	Glia activating fa
51	16	7.6	207	22	AAU02080	Glia activating fa
52	16	7.6	207	22	AAU02080	Glia activating fa
53	11	5.2	61	17	AAU02080	Glia activating fa
54	10	4.7	14	18	AAU02080	Glia activating fa
55	9	4.3	27	16	AAU02080	Glia activating fa
56	8	3.8	76	22	AAU02080	Glia activating fa
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59	8	3.8	318	22	AAU02080	Glia activating fa
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61	7	3.3	42	22	AAU02080	Glia activating fa
62	7	3.3	42	22	AAU02080	Glia activating fa
63	7	3.3	42	22	AAU02080	Glia activating fa
64	7	3.3	42	22	AAU02080	Glia activating fa
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69	7	3.3	74	22	AAU02080	Glia activating fa
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71	7	3.3	86	21	AAU02080	Glia activating fa
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73	7	3.3	106	21	AAU02080	Glia activating fa
74	7	3.3	106	21	AAU02080	Glia activating fa
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78	7	3.3	124	21	AAU02080	Glia activating fa
79	7	3.3	136	21	AAU02080	Glia activating fa
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81	7	3.3	136	22	AAU02080	Glia activating fa
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83	7	3.3	138	21	AAU02080	Glia activating fa
84	7	3.3	141	21	AAU02080	Glia activating fa

85	7	3.3	145	20	AA37604	Protein which is s	158	7	3.3	711	20	AAW86021	Human lactoferrin
86	7	3.3	158	22	AA33271	Human protein sequ	159	7	3.3	711	21	AAW86021	Amino acid sequenc
87	7	3.3	174	22	AA40400	Human polypeptide	160	7	3.3	711	21	AAW86021	Human lactoferrin
88	7	3.3	181	19	AAW39181	Human PKD1 protein	161	7	3.3	711	21	AAW77578	Human lactoferrin
89	7	3.3	189	22	AAW42186	Human polypeptide	162	7	3.3	711	22	AAW42186	Chronic hepatitis
90	7	3.3	201	19	AAW39182	Human PKD1 protein	163	7	3.3	711	22	AAE02341	Human lactoferrin
91	7	3.3	217	22	ABG23027	Novel human diagno	164	7	3.3	711	22	AAW36843	Human lactoferrin
92	7	3.3	224	21	AA444967	Human taste cell s	165	7	3.3	732	21	AAW49928	Arabidopsis thalia
93	7	3.3	233	21	AAW30097	Arabidopsis thalia	166	7	3.3	738	21	AAW49927	Arabidopsis thalia
94	7	3.3	236	21	AAW30096	Arabidopsis thalia	167	7	3.3	738	21	AAW49926	Arabidopsis thalia
95	7	3.3	239	21	AAW30095	Arabidopsis thalia	168	7	3.3	757	22	AAU03497	Human sterol sensi
96	7	3.3	244	21	AAW09812	Arabidopsis thalia	169	7	3.3	758	21	AAW41293	Human ORFX ORF1057
97	7	3.3	258	21	AAW47700	Arabidopsis thalia	170	7	3.3	763	21	AAW42390	Arabidopsis thalia
98	7	3.3	260	20	AA137417	Amino acid sequenc	171	7	3.3	766	21	AAW42388	Arabidopsis thalia
99	7	3.3	262	21	AAW32123	Arabidopsis thalia	172	7	3.3	772	21	AAW42388	Drosophila melanog
100	7	3.3	266	22	ABG05763	Novel human diagno	173	7	3.3	783	22	ABW71349	Large subunit of p
101	7	3.3	282	19	AAW64461	Human secreted pro	174	7	3.3	853	21	ABW71349	Novel human diagno
102	7	3.3	323	19	AAW93897	Human protein sequ	175	7	3.3	1003	22	ABG23021	Serum opacity fact
103	7	3.3	333	22	AAW93897	Human protein sequ	176	7	3.3	1025	16	AAW70126	Novel human diagno
104	7	3.3	357	19	AAW72100	HSV-2 strain SB5 C	177	7	3.3	1028	22	ABG15393	Drosophila melanog
105	7	3.3	364	21	AAW35260	HSV-2 strain SB5 C	178	7	3.3	1058	22	ABW62096	Drosophila melanog
106	7	3.3	364	21	AAW35260	HSV-2 strain SB5 C	179	7	3.3	1120	22	ABW68196	C glutamic prote
107	7	3.3	373	22	AAW40200	Human polypeptide	180	7	3.3	1233	22	AAW90558	Novel human diagno
108	7	3.3	381	21	AAW35259	Zea mays protein f	181	7	3.3	1235	22	ABG17056	Novel human diagno
109	7	3.3	384	21	AAW71056	Zea mays protein f	182	7	3.3	1270	22	ABG17056	Novel human diagno
110	7	3.3	384	22	AAW40198	Human membrane tra	183	7	3.3	1355	22	ABW63317	Drosophila melanog
111	7	3.3	384	22	AAW40198	Human polypeptide	184	7	3.3	1579	22	ABW63317	Novel human diagno
112	7	3.3	388	21	AAW35259	Zea mays protein f	185	7	3.3	1614	16	AAW75917	Drosophila melanog
113	7	3.3	391	22	ABW67472	Amino acid sequenc	186	7	3.3	1614	16	AAW75917	Polycystic kidney
114	7	3.3	414	22	AAW78215	Human MAP kinase i	187	7	3.3	3313	22	AAU30134	Novel human secret
115	7	3.3	424	18	AAW23818	Arabidopsis floral	188	7	3.3	3390	22	AAE07999	Wild-type, virulen
116	7	3.3	424	19	AAW45512	Arabidopsis floral	189	7	3.3	3390	22	AAE07999	Attenuated, vaccin
117	7	3.3	424	19	AAW43332	Arabidopsis floral	190	7	3.3	3439	16	AAW75916	Polycystic kidney
118	7	3.3	424	21	AAW39138	Amino acid sequenc	191	7	3.3	4292	17	AAW00870	Polycystic kidney
119	7	3.3	424	21	AAW19248	Human polypeptide	192	7	3.3	4302	19	AAW33396	Human PKD1 polypep
120	7	3.3	424	21	AAW78886	A. thaliana LFY pr	193	7	3.3	4302	19	AAW23830	Human PKD1 protein
121	7	3.3	458	22	AAU31109	Novel human secret	194	7	3.3	4302	21	AAW23830	Human polycystin
122	7	3.3	469	22	AAW42077	Novel human neopla	195	7	3.3	4303	17	AAW90302	Polycystic kidney
123	7	3.3	567	22	AAU21696	Drosophila melanog	196	7	3.3	4339	16	AAW75916	Polycystic kidney
124	7	3.3	631	22	ABW69813	Human protein sequ	197	7	3.3	4339	17	AAW75916	Polycystic kidney
125	7	3.3	637	22	AAW94689	Human polycystic d	198	7	3.3	4725	22	ABG23837	Novel human diagno
126	7	3.3	643	22	ABW11071	Novel human diagno	199	7	3.3	4725	22	ABG17057	Novel human diagno
127	7	3.3	671	22	ABG17058	Novel human diagno	200	7	3.3	4725	22	ABG17057	Novel human diagno
128	7	3.3	678	22	ABW58061	Drosophila melanog	201	7	3.3	6685	22	ABG23030	Rat fibroblast gro
129	7	3.3	687	22	AAW71183	Mutant human lacto	202	6	2.8	6	22	AAU02085	Rat fibroblast gro
130	7	3.3	687	22	AAW71183	Human lactoferrin	203	6	2.8	6	22	AAU02086	Rat fibroblast gro
131	7	3.3	688	19	AAW71182	Mutant human lacto	204	6	2.8	6	22	AAU02087	Rat fibroblast gro
132	7	3.3	688	22	AAW71182	Human lactoferrin	205	6	2.8	6	22	AAU02088	Flavoprotein Epid
133	7	3.3	688	22	AAW71182	Human lactoferrin	206	6	2.8	8	20	AAW43458	Procollagen alpha
134	7	3.3	689	22	AAW71181	Mutant human lacto	207	6	2.8	10	22	AAW93400	Amino acid sequenc
135	7	3.3	689	22	AAW71181	Human lactoferrin	208	6	2.8	10	22	AAW93400	Vaccine related MH
136	7	3.3	690	22	AAW71180	Mutant human lacto	209	6	2.8	11	19	AAW59848	Sequence of beta-D
137	7	3.3	690	22	AAW71180	Human lactoferrin	210	6	2.8	14	22	AAW98915	Amino acid sequenc
138	7	3.3	692	21	AAW58733	Human lactoferrin	211	6	2.8	15	19	AAW59853	HLA-A2-binding HIV
139	7	3.3	692	22	AAW77906	Human lactoferrin	212	6	2.8	15	21	AAW66451	Peptide #4792 enco
140	7	3.3	692	22	AAW97382	Lactoferrin protel	213	6	2.8	17	22	AAW70520	Peptide #4641 enco
141	7	3.3	693	16	AAW85146	Human lactoferrin	214	6	2.8	17	22	AAW70520	Peptide #11780 enc
142	7	3.3	705	13	AAW22423	Human lactoferrin	215	6	2.8	25	22	ABW44274	Tryptic peptide fr
143	7	3.3	705	20	AAW31152	Human lactoferrin	216	6	2.8	25	22	AAW05959	Human secreted pro
144	7	3.3	708	13	AAW22424	Human lactoferrin	217	6	2.8	26	22	ABW50711	Human colon cancer
145	7	3.3	708	20	AAW31153	Human lactoferrin	218	6	2.8	26	22	ABW50711	pl8 of nef peptide
146	7	3.3	709	15	AAW45199	Human lactoferrin	219	6	2.8	29	22	AAW77091	Human polypeptide
147	7	3.3	709	15	AAW45198	Human lactoferrin	220	6	2.8	31	14	AAW42699	Peptide PF18 from
148	7	3.3	709	18	AAW21695	Human lactoferrin	221	6	2.8	32	22	AAW07983	Human polypeptide
149	7	3.3	709	19	AAW53879	Human lactoferrin	222	6	2.8	33	10	AAW92272	Human colon cancer
150	7	3.3	709	21	AAW03830	Human lactoferrin	223	6	2.8	33	22	AAW75761	Human polypeptide
151	7	3.3	709	21	AAW77577	Protein encoded by	224	6	2.8	34	22	AAW09532	Superantigen pepti
152	7	3.3	709	22	AAW36842	Human lactoferrin	225	6	2.8	34	22	AAW09532	HIV Negative facto
153	7	3.3	711	11	AAW08033	Lactoferrin, Homo	226	6	2.8	40	16	AAW74070	Human secreted pro
154	7	3.3	711	14	AAW43653	Human lactoferrin	227	6	2.8	40	20	AAW39989	Cytomegalovirus la
155	7	3.3	711	17	AAW09342	Human lactoferrin	228	6	2.8	41	21	AAW91544	
156	7	3.3	711	19	AAW57317	Human lactoferrin	229	6	2.8	42	18	AAW06501	
157	7	3.3	711	19	AAW53880	Bovine alphaS1-cas	230	6	2.8	42	18	AAW06501	

231	6	2.8	43	22	ABB39963	Peptide #7469 enco	304	2.8	80	21	ABG04361	Arabidopsis thalia
232	6	2.8	43	22	ABB24497	Protein #6496 enco	305	2.8	80	22	ABG17801	Novel human thalia
233	6	2.8	43	22	AAAM60708	Human brain expres	306	2.8	80	22	ABG11126	Human secreted pro
234	6	2.8	43	22	AAAM73581	Human bone marrow	307	2.8	82	20	AAAY12445	Human 5' EST secre
235	6	2.8	43	22	AAAM33583	Peptide #7620 enco	308	2.8	83	13	AAAR28992	Encoded by human G
236	6	2.8	46	14	AAAR42695	p14 of nef peptide	309	2.8	83	16	AAAR94760	nef CTL1 epitope d
237	6	2.8	47	20	AAAY12851	Human 5' EST secre	310	2.8	83	22	ABBI7990	Human nervous syst
238	6	2.8	48	10	AAAP92268	Peptide pF14 from	311	2.8	83	22	AAAB88619	Human immune/haema
239	6	2.8	49	22	ABBA1227	Peptide #8733 enco	312	2.8	83	22	AAAB98916	HIV Nef-1 CTL epit
240	6	2.8	49	22	ABBA25233	Protein #7232 enco	313	2.8	84	22	ABG12684	Novel human thalia
241	6	2.8	49	22	AAAM62091	Human brain expres	314	2.8	86	22	AAAB83146	Human immune/haema
242	6	2.8	49	22	AAAM74893	Human bone marrow	315	2.8	87	20	AAAY60427	Human normal bladd
243	6	2.8	49	22	AAAM35009	Peptide #9046 enco	316	2.8	88	22	AAAG75581	Human colon cancer
244	6	2.8	52	22	AAAU43770	Propionibacterium	317	2.8	88	22	AAUG66908	Propionibacterium
245	6	2.8	54	22	AAAU49248	Propionibacterium	318	2.8	89	22	AAUG65512	Propionibacterium
246	6	2.8	55	22	AAAU43205	Propionibacterium	319	2.8	89	22	ABG26496	Novel human thalia
247	6	2.8	55	22	ABBB30939	Peptide #3590 enco	320	2.8	90	22	AAU56667	Propionibacterium
248	6	2.8	55	22	ABBB36129	Peptide #3635 enco	321	2.8	91	22	AAU59395	Propionibacterium
249	6	2.8	55	22	ABBB21514	Protein #3513 enco	322	2.8	93	21	AAAG04360	Arabidopsis thalia
250	6	2.8	55	22	AAU21172	Human novel foetal	323	2.8	96	21	AAAG27221	zea mays protein f
251	6	2.8	55	22	AAAM56912	Human brain expres	324	2.8	96	22	AAU43245	Propionibacterium
252	6	2.8	55	22	AAAM69300	Human bone marrow	325	2.8	96	22	AAU57327	Propionibacterium
253	6	2.8	55	22	AAAM17125	Peptide #3559 enco	326	2.8	96	22	AAAG67744	Amino acid sequenc
254	6	2.8	55	22	AAAM29619	Peptide #3656 enco	327	2.8	96	22	AAO05429	Human polypeptide
255	6	2.8	56	22	AAU58509	Propionibacterium	328	2.8	97	21	AAAG58758	Arabidopsis thalia
256	6	2.8	56	22	ABG01841	Novel human thalia	329	2.8	97	22	AAU46317	Propionibacterium
257	6	2.8	56	22	ABG01842	Novel human thalia	330	2.8	99	21	AAAG16013	Arabidopsis thalia
258	6	2.8	57	22	AAAB92434	Miscellaneous pept	331	2.8	99	22	AAAG63913	Propionibacterium
259	6	2.8	58	22	AAU60226	Propionibacterium	332	2.8	100	21	AAAB59093	Breast and ovarian
260	6	2.8	60	22	AAAE00643	Human fibroblast g	333	2.8	100	21	AAAB41525	Human ORFX ORF1289
261	6	2.8	61	20	AAAY12082	Human 5' EST secre	334	2.8	102	21	AAAG16012	Arabidopsis thalia
262	6	2.8	61	22	ABBI1863	Human cathepsin L	335	2.8	102	22	ABBI6216	Human nervous syst
263	6	2.8	62	20	AAAY11669	Human 5' EST secre	336	2.8	103	21	AAAG13823	Arabidopsis thalia
264	6	2.8	62	22	AAU44829	Propionibacterium	337	2.8	103	22	AAAB8927	Human immune/haema
265	6	2.8	64	22	AAAB61989	Propionibacterium	338	2.8	103	22	AAAB66011	Human secreted pro
266	6	2.8	64	22	ABBB29595	Peptide #2246 enco	339	2.8	104	22	AAO25689	G protein-coupled
267	6	2.8	64	22	ABBB34775	Peptide #2281 enco	340	2.8	105	22	AAO10255	Human polypeptide
268	6	2.8	64	22	ABBB20190	Protein #2189 enco	341	2.8	106	14	AAAR36386	Urease beta subuni
269	6	2.8	64	22	AAAB55577	Human brain expres	342	2.8	106	22	AAAR92785	Human digestive sy
270	6	2.8	64	22	AAAB65652	Human brain expres	343	2.8	106	22	AAAB94685	Human protein sequ
271	6	2.8	64	22	AAAB67959	Human bone marrow	344	2.8	108	21	AAAG16011	Arabidopsis thalia
272	6	2.8	64	22	AAAM78268	Peptide #2212 enco	345	2.8	108	21	AAAG58757	Arabidopsis thalia
273	6	2.8	64	22	AAAM15778	Peptide #2325 enco	346	2.8	109	21	AAAG24511	Arabidopsis thalia
274	6	2.8	64	22	AAAM28288	Peptide #2195 enco	347	2.8	109	22	ABG24079	Novel human thalia
275	6	2.8	66	21	AAAM03513	Arabidopsis thalia	348	2.8	110	21	AAAG24510	Arabidopsis thalia
276	6	2.8	66	21	AAAG04362	Human EST encoded	349	2.8	110	22	ABB50710	Human secreted pro
277	6	2.8	66	22	AAAM23882	Human EST encoded	350	2.8	110	22	AAAB84713	Human immune/haema
278	6	2.8	68	17	AAAR81547	Promersacidin lant	351	2.8	110	22	AAAM25787	Human protein sequ
279	6	2.8	68	22	AAAM80077	Human protein SEQ	352	2.8	111	22	AAU43579	Propionibacterium
280	6	2.8	70	21	AAAB18677	Peptide fragment f	353	2.8	111	22	AAAG81511	S. epidermidis Ope
281	6	2.8	70	21	AAAB18679	Mutant peptide der	354	2.8	111	22	AAAB50300	Human fibroblast g
282	6	2.8	70	21	AAAB18680	Mutant peptide der	355	2.8	112	22	AAAB83853	Human immune/haema
283	6	2.8	70	21	AAAB18681	Mutant peptide der	356	2.8	112	20	AAAY14141	zea mays SCLBR pro
284	6	2.8	70	21	AAAB18682	Mutant peptide der	357	2.8	114	21	AAAG13822	Arabidopsis thalia
285	6	2.8	70	21	AAAB18683	Mutant peptide der	358	2.8	115	21	AAU47801	Propionibacterium
286	6	2.8	70	21	AAAB18684	Mutant peptide der	359	2.8	117	22	AAU53166	Propionibacterium
287	6	2.8	70	21	AAAB18685	Mutant peptide der	360	2.8	118	21	AAAG24509	Arabidopsis thalia
288	6	2.8	70	21	AAAB18686	Mutant peptide der	361	2.8	119	22	AAAM41833	Human polypeptide
289	6	2.8	70	21	AAAB18688	Mutant peptide der	362	2.8	120	21	AAAB43106	Human ORFX ORF2870
290	6	2.8	70	21	AAAB18689	Mutant peptide der	363	2.8	120	22	AAU32167	Novel human secret
291	6	2.8	70	21	AAAB18690	Mutant peptide der	364	2.8	121	19	AAAW23892	Murine fibroblast
292	6	2.8	70	21	AAAB18691	Mutant peptide der	365	2.8	121	21	AAAY97888	Rat fibroblast gro
293	6	2.8	70	21	AAAB18692	Mutant peptide der	366	2.8	121	22	AAAM61270	Human brain expres
294	6	2.8	70	21	AAAY91690	Human secreted pro	367	2.8	121	22	AAAM73993	Human bone marrow
295	6	2.8	70	22	ABG25882	Novel human thalia	368	2.8	121	22	AAU17273	Novel signal trans
296	6	2.8	71	20	AAAY05629	HIV-1 group O isol	369	2.8	122	10	AAAP93697	Protein encoded by
297	6	2.8	73	22	AAU633369	Propionibacterium	370	2.8	122	16	AAAR75407	HIV-3 strain AMT70
298	6	2.8	73	22	AAU63962	Propionibacterium	371	2.8	122	20	AAAY36111	Extended human sec
299	6	2.8	75	20	AAAY48581	Human breast tumou	372	2.8	122	22	ABG22209	Novel human thalia
300	6	2.8	75	22	AAU54326	Propionibacterium	373	2.8	123	19	AAAB23891	Human fibroblast g
301	6	2.8	76	22	ABBI15813	Human nervous syst	374	2.8	123	22	AAAB80395	Secreted protein e
302	6	2.8	78	22	AAU41559	Propionibacterium	375	2.8	123	22	AAAB86000	Amino acid sequenc
303	6	2.8	79	22	AAU47735	Propionibacterium	376	2.8	125	22	ABG27466	Novel human thalia

377	6	2.8	125	22	AAG73819	Human colon cancer	450	6	2.8	177	12	AAR12787	Non-glycosylated f
378	6	2.8	126	22	AAM90373	Human immune/haema	451	6	2.8	177	21	AAG08237	Arabidopsis thalia
379	6	2.8	127	22	AAU43595	Propionibacterium	452	6	2.8	178	21	AAB41654	Human ORFX ORF1418
380	6	2.8	127	22	AAU54171	Propionibacterium	453	6	2.8	178	21	AAG08236	Arabidopsis thalia
381	6	2.8	127	22	AAU65852	Propionibacterium	454	6	2.8	178	22	AU020429	Human secreted pro
382	6	2.8	127	22	AAU63585	Human polypeptide,	455	6	2.8	182	22	ABU68284	Drosophila melanog
383	6	2.8	128	21	AAG01030	Human polypeptide,	456	6	2.8	182	22	AAU39281	Human polypeptide
384	6	2.8	128	21	AAY95014	Human secreted pro	457	6	2.8	182	22	AAU19434	Human diagnostic a
385	6	2.8	129	10	AAU91577	Human secreted pro	458	6	2.8	183	22	ABU12276	Human secretory pr
386	6	2.8	129	21	AAB42396	Sequence of electr	459	6	2.8	183	22	AAU33554	Human protein sequ
387	6	2.8	129	21	AAU51200	Human ORFX ORF2160	460	6	2.8	185	22	AAU18526	Human cytoskeletal
388	6	2.8	129	22	AAU00853	Human SCF7 protein	461	6	2.8	186	22	ABU10962	Novel human diago
389	6	2.8	131	22	ABU64217	Human bone marrow	462	6	2.8	186	22	ABU87419	Human gene 3 encod
390	6	2.8	131	22	ABU64217	Drosophila melanog	463	6	2.8	187	21	AAU42918	Human ORFX ORF2682
391	6	2.8	132	21	AAU81275	Novel human diago	464	6	2.8	189	21	AAU16513	Arabidopsis thalia
392	6	2.8	132	21	AAU81275	Mature M13 coat pr	465	6	2.8	189	22	AAU42341	Propionibacterium
393	6	2.8	133	21	AAU81275	Arabidopsis thalia	466	6	2.8	189	22	ABU25347	Novel human diago
394	6	2.8	133	21	AAU81275	Arabidopsis thalia	467	6	2.8	191	22	AAU39671	Human polypeptide
395	6	2.8	133	22	AAU81275	Arabidopsis thalia	468	6	2.8	191	22	AAU39671	Human protein sequ
396	6	2.8	133	22	AAU81275	Propionibacterium	469	6	2.8	192	22	AAU39279	Human polypeptide
397	6	2.8	133	22	AAU81275	Human polypeptide	470	6	2.8	195	22	AAU39279	Human protein sequ
398	6	2.8	133	22	AAU81275	Mycobacterium tube	471	6	2.8	196	22	AAU39279	S. pneumoniae deri
399	6	2.8	134	21	AAU81275	Zea mays protein f	472	6	2.8	196	22	AAU39279	Novel human diago
400	6	2.8	134	22	AAU81275	Propionibacterium	473	6	2.8	196	22	AAU39279	Human protein sequ
401	6	2.8	136	22	AAU36591	Staphylococcus aur	474	6	2.8	196	22	AAU39279	Novel human diago
402	6	2.8	137	21	AAU36591	Arabidopsis thalia	475	6	2.8	197	22	AAU39279	Human polypeptide
403	6	2.8	137	22	AAU36591	Arabidopsis thalia	476	6	2.8	198	16	AAU39279	Human protein sequ
404	6	2.8	138	18	AAU20425	Novel human diago	477	6	2.8	198	16	AAU39279	Human polypeptide
405	6	2.8	138	18	AAU20425	H. pylori inner me	478	6	2.8	198	16	AAU39279	Human protein sequ
406	6	2.8	138	18	AAU20425	H. pylori inner me	479	6	2.8	198	16	AAU39279	S. pneumoniae deri
407	6	2.8	138	20	AAU12378	Human 5' EST secre	480	6	2.8	198	16	AAU39279	Novel human diago
408	6	2.8	139	22	AAU12378	Human cDNA SEQ ID	481	6	2.8	198	21	AAU39279	Human protein sequ
409	6	2.8	140	15	AAU45439	Truncated K-FGF,	482	6	2.8	198	21	AAU39279	Novel human diago
410	6	2.8	141	22	AAU63931	Propionibacterium	483	6	2.8	199	22	AAU63931	Human polypeptide
411	6	2.8	141	22	AAU63931	Human polypeptide	484	6	2.8	199	22	AAU63931	Human polypeptide
412	6	2.8	142	22	AAU63931	Human signal pepti	485	6	2.8	199	22	AAU63931	Novel human diago
413	6	2.8	142	22	AAU63931	Human gene 6 encod	486	6	2.8	199	22	AAU63931	S. epidermidis ope
414	6	2.8	143	22	AAU63931	Human protein sequ	487	6	2.8	201	21	AAU63931	Neisseria gonorrhoe
415	6	2.8	146	15	AAU63931	Mutant heparin-bin	488	6	2.8	201	22	AAU63931	Human polypeptide
416	6	2.8	146	21	AAU63931	Human colon cancer	489	6	2.8	202	22	AAU63931	Human polypeptide
417	6	2.8	146	22	AAU63931	Propionibacterium	490	6	2.8	202	22	AAU63931	Fibroblast growth
418	6	2.8	147	12	AAU11464	Hst-1 mutain N27.	491	6	2.8	202	22	AAU63931	Murine fibroblast
419	6	2.8	147	22	AAU74930	Human colon cancer	492	6	2.8	202	22	AAU63931	Rat KGF protein.
420	6	2.8	148	13	AAU21608	Human colon cancer	493	6	2.8	203	22	AAU63931	C. glutamicum prote
421	6	2.8	148	13	AAU21608	Heparin binding se	494	6	2.8	203	22	AAU63931	Novel human secret
422	6	2.8	148	13	AAU21608	Sequence of mutain	495	6	2.8	204	22	AAU63931	Human EGF-4 protei
423	6	2.8	150	21	AAU63931	Human prostate can	496	6	2.8	205	21	AAU63931	Sequence of E' pro
424	6	2.8	152	21	AAU63931	Arabidopsis thalia	497	6	2.8	206	7	AAU63931	Nef protein of HIV
425	6	2.8	153	21	AAU63931	Human ORFX ORF807	498	6	2.8	206	14	AAU63931	Sequence of hepari
426	6	2.8	153	22	AAU63931	Novel human secret	499	6	2.8	206	16	AAU63931	Fibroblast growth
427	6	2.8	154	15	AAU63931	Murine protein tyr	500	6	2.8	206	16	AAU63931	Fibroblast growth
428	6	2.8	156	22	AAU42675	Propionibacterium	501	6	2.8	206	16	AAU63931	FGF-4. Homo sapie
429	6	2.8	157	22	AAU42675	Human haematologic	502	6	2.8	206	19	AAU63931	Fibroblast growth
430	6	2.8	157	22	AAU42675	Human secreted pro	503	6	2.8	206	19	AAU63931	HTLV-III E' protei
431	6	2.8	159	21	AAU63931	Human colon cancer	504	6	2.8	206	20	AAU63931	HIV-1 nef protein
432	6	2.8	160	20	AAU63931	Human colon cancer	505	6	2.8	206	20	AAU63931	HIV-1 non-subtype
433	6	2.8	160	20	AAU63931	Ehrlichia sp. E74.	506	6	2.8	206	21	AAU63931	HIV-1 non-subtype
434	6	2.8	161	13	AAU24301	Glycopeptide resis	507	6	2.8	206	21	AAU63931	Fibroblast growth
435	6	2.8	161	13	AAU24301	Propionibacterium	508	6	2.8	206	21	AAU63931	HIV-1 nef protein.
436	6	2.8	163	22	AAU96132	Putative 3-isoprop	509	6	2.8	206	21	AAU63931	FGF-4, SEQ ID NO:1
437	6	2.8	163	22	AAU96132	Human immunoglobul	510	6	2.8	206	21	AAU63931	Human fibroblast g
438	6	2.8	163	22	AAU96132	Human secreted pro	511	6	2.8	206	21	AAU63931	Human NEF protein/
439	6	2.8	168	21	AAU28962	Arabidopsis thalia	512	6	2.8	206	22	AAU63931	Human fibroblast g
440	6	2.8	169	22	AAU63676	Human gastric canc	513	6	2.8	206	22	AAU63931	Human fibroblast g
441	6	2.8	170	22	AAU63676	Novel human diago	514	6	2.8	206	22	AAU63931	FGF4 protein. Hom
442	6	2.8	171	15	AAU63676	Mutant heparin-bin	515	6	2.8	206	22	AAU63931	Human RGF-4 SQ ID
443	6	2.8	171	15	AAU63676	Novel human diago	516	6	2.8	206	22	AAU63931	Human fibroblast g
444	6	2.8	175	13	AAU63676	Heparin binding se	517	6	2.8	206	22	AAU63931	Sequence deduced f
445	6	2.8	175	15	AAU63676	Sequence of mature	518	6	2.8	207	11	AAU63931	HIV-1 non-subtype
446	6	2.8	175	15	AAU63676	Heparin-binding se	519	6	2.8	207	11	AAU63931	Human RGF-6 protei
447	6	2.8	175	22	AAU79750	C. glutamicum meta	520	6	2.8	207	13	AAU79750	HST2 protein encod
448	6	2.8	175	22	AAU79750	Corynebacterium gl	521	6	2.8	208	13	AAU79750	Heparin-binding se
449	6	2.8	175	22	AAU79750	Corynebacterium gl	522	6	2.8	208	15	AAU79750	HIV-1 non-subtype
	6	2.8	176	22	AAU79750	Human fibroblast g		6	2.8	208	15	AAU79750	
	6	2.8	176	22	AAU79750	Human fibroblast g		6	2.8	208	21	AAU79750	

523	6	2.8	208	22	ABB69265	Drosophila melanog	596	6	2.8	248	20	AAV31791	Human fibroblast g
524	6	2.8	208	22	ABG65652	Human fibroblast g	597	6	2.8	248	21	AAB53418	Human colon cancer
525	6	2.8	208	22	AAB85817	Human fibroblast g	598	6	2.8	252	22	AAB61133	Human NOV5 protein
526	6	2.8	208	22	AAB85835	Murine fibroblast	599	6	2.8	252	22	AAB61134	Human NOV21 protei
527	6	2.8	208	22	AAB50278	Human FGF-6 SEQ ID	600	6	2.8	252	22	AAB61135	Human NOV22 protei
528	6	2.8	208	22	AAB50708	Human fibroblast g	601	6	2.8	255	21	AAB24698	Human ORFX ORF2462
529	6	2.8	208	22	AAB50708	Human fibroblast g	602	6	2.8	257	20	AAV35468	Chlamydia pneumoni
530	6	2.8	209	21	AAB43342	Human ORFX ORF3106	603	6	2.8	257	22	ABG29649	Novel human diagno
531	6	2.8	209	21	AAG12935	Arabidopsis thalia	604	6	2.8	257	22	AAE03368	Human gene 16 enco
532	6	2.8	209	21	AAG53253	Arabidopsis thalia	605	6	2.8	259	22	ABG63173	Drosophila melanog
533	6	2.8	209	22	ABB11088	Human sialic acid	606	6	2.8	260	21	AAV70244	Human RNA-associat
534	6	2.8	210	12	AAR12262	HIV-1 strain Orl o	607	6	2.8	260	22	ABBS0208	Human transcriptio
535	6	2.8	210	19	AAW53119	Protein 6 containe	608	6	2.8	260	22	ABBS0208	Human transcriptio
536	6	2.8	210	21	AAV77299	HIV-1 (ATCC CRL 85	609	6	2.8	261	22	ABBS0208	Human transcriptio
537	6	2.8	210	22	AAW41065	Human polypeptide	610	6	2.8	261	22	ABBS0208	Human transcriptio
538	6	2.8	210	22	AAW41066	Human polypeptide	611	6	2.8	261	22	ABBS0208	Human transcriptio
539	6	2.8	210	22	AAW41067	Human polypeptide	612	6	2.8	262	22	ABBS0208	Human transcriptio
540	6	2.8	210	22	AAW68481	HIV-1 strain YBF30	613	6	2.8	265	22	ABBS0208	Human transcriptio
541	6	2.8	212	19	AAW68481	Polypeptide fragme	614	6	2.8	265	22	ABBS0208	Human transcriptio
542	6	2.8	212	20	AAW01198	Propionibacterium	615	6	2.8	265	22	ABBS0208	Human transcriptio
543	6	2.8	214	22	AAU41669	A representative H	616	6	2.8	266	20	AAW41098	Drosophila melanog
544	6	2.8	215	20	AAU02349	Propionibacterium	617	6	2.8	266	21	AAW41098	Drosophila melanog
545	6	2.8	215	22	AAW63231	Amino acid sequenc	618	6	2.8	266	21	AAW41098	Drosophila melanog
546	6	2.8	216	7	AAW60423	Sequence of LAV vi	619	6	2.8	266	21	AAW41098	Drosophila melanog
547	6	2.8	216	22	AAE04960	HIV-1 jrf1 Nef pro	620	6	2.8	266	21	AAW41098	Drosophila melanog
548	6	2.8	217	22	AAE04962	HIV-1 jrf1 Nef (G2	621	6	2.8	266	21	AAW41098	Drosophila melanog
549	6	2.8	217	22	AAU01268	Brassica napus fat	622	6	2.8	266	21	AAW41098	Drosophila melanog
550	6	2.8	220	22	AAW41456	Human polypeptide	623	6	2.8	267	14	AAW41098	Drosophila melanog
551	6	2.8	220	22	AAW41457	Human polypeptide	624	6	2.8	267	18	AAW41098	Drosophila melanog
552	6	2.8	224	21	AAW44601	Maize MfO1 protein	625	6	2.8	267	22	AAW41098	Drosophila melanog
553	6	2.8	224	21	AAW86197	Nuclear transport	626	6	2.8	267	22	AAW41098	Drosophila melanog
554	6	2.8	225	21	AAW12934	Arabidopsis thalia	627	6	2.8	267	22	AAW41098	Drosophila melanog
555	6	2.8	225	21	AAW53252	Arabidopsis thalia	628	6	2.8	267	22	AAW41098	Drosophila melanog
556	6	2.8	226	22	AAU33952	Staphylococcus aur	629	6	2.8	267	22	AAW41098	Drosophila melanog
557	6	2.8	226	22	AAW79581	Human protein SEQ	630	6	2.8	268	16	AAW41098	Drosophila melanog
558	6	2.8	229	21	AAW58846	Breast and ovarian	631	6	2.8	268	16	AAW41098	Drosophila melanog
559	6	2.8	230	20	AAW36134	Human secreted pro	632	6	2.8	268	19	AAW41098	Drosophila melanog
560	6	2.8	230	20	AAW36181	Human secreted pro	633	6	2.8	268	19	AAW41098	Drosophila melanog
561	6	2.8	230	21	AAW06849	Arabidopsis thalia	634	6	2.8	268	20	AAW41098	Drosophila melanog
562	6	2.8	230	21	AAW99378	Human PRO1356 (UNQ	635	6	2.8	268	20	AAW41098	Drosophila melanog
563	6	2.8	230	21	AAW84609	A human membrane	636	6	2.8	268	20	AAW41098	Drosophila melanog
564	6	2.8	230	21	AAW51676	Murine clodin 2 pr	637	6	2.8	268	21	AAW41098	Drosophila melanog
565	6	2.8	230	22	AAW09178	Human PRO1356 poly	638	6	2.8	268	21	AAW41098	Drosophila melanog
566	6	2.8	230	22	AAU17194	Novel signal trans	639	6	2.8	268	21	AAW41098	Drosophila melanog
567	6	2.8	230	22	AAW38857	Human polypeptide	640	6	2.8	268	22	AAW41098	Drosophila melanog
568	6	2.8	230	22	AAU12417	Human PRO1356 poly	641	6	2.8	268	22	AAW41098	Drosophila melanog
569	6	2.8	230	22	AAE04207	Human gene 10 enco	642	6	2.8	268	22	AAW41098	Drosophila melanog
570	6	2.8	230	22	AAW87565	Human PRO1356. Ho	643	6	2.8	268	22	AAW41098	Drosophila melanog
571	6	2.8	230	22	AAW88342	Human membrane or	644	6	2.8	268	22	AAW41098	Drosophila melanog
572	6	2.8	230	22	AAW66127	Protein of the inv	645	6	2.8	268	22	AAW41098	Drosophila melanog
573	6	2.8	231	21	AAW43861	Human cancer assoc	646	6	2.8	269	21	AAW41098	Drosophila melanog
574	6	2.8	231	22	AAU16339	Human novel secret	647	6	2.8	270	21	AAW41098	Drosophila melanog
575	6	2.8	231	22	AAW75629	Human colon cancer	648	6	2.8	270	22	AAW41098	Drosophila melanog
576	6	2.8	233	21	AAW58878	Breast and ovarian	649	6	2.8	270	22	AAW41098	Drosophila melanog
577	6	2.8	235	11	AAW05209	Human contig polyp	650	6	2.8	271	22	AAW41098	Drosophila melanog
578	6	2.8	236	11	AAW05209	yeast Ubiquitin hy	651	6	2.8	271	22	AAW41098	Drosophila melanog
579	6	2.8	236	22	AAU30086	Novel human secret	652	6	2.8	273	21	AAW41098	Drosophila melanog
580	6	2.8	236	22	AAU30098	Novel human secret	653	6	2.8	273	22	AAW41098	Drosophila melanog
581	6	2.8	237	16	AAW74336	Helicobacter felis	654	6	2.8	273	22	AAW41098	Drosophila melanog
582	6	2.8	237	17	AAW06729	H. felis structura	655	6	2.8	273	22	AAW41098	Drosophila melanog
583	6	2.8	237	22	AAW06729	Novel human diagno	656	6	2.8	273	22	AAW41098	Drosophila melanog
584	6	2.8	237	22	AAE04961	Human tPA leader p	657	6	2.8	273	22	AAW41098	Drosophila melanog
585	6	2.8	237	22	AAE04963	Human tPA leader p	658	6	2.8	275	20	AAW41098	Drosophila melanog
586	6	2.8	238	18	AAW32796	Esterase protein E	659	6	2.8	275	22	AAW41098	Drosophila melanog
587	6	2.8	238	22	AAW61538	Degr protease. St	660	6	2.8	276	21	AAW41098	Drosophila melanog
588	6	2.8	245	21	AAW92819	C. pneumoniae CPN1	661	6	2.8	277	20	AAW41098	Drosophila melanog
589	6	2.8	245	22	ABBS5290	Drosophila melanog	662	6	2.8	278	22	AAW41098	Drosophila melanog
590	6	2.8	245	22	AAU56269	Propionibacterium	663	6	2.8	278	22	AAW41098	Drosophila melanog
591	6	2.8	245	22	ABG03592	Novel human diagno	664	6	2.8	279	22	ABBS5447	Drosophila melanog
592	6	2.8	246	22	AAW59389	Human protein tyro	665	6	2.8	279	22	ABBS5447	Drosophila melanog
593	6	2.8	246	22	AAE00639	Human fibroblast g	666	6	2.8	280	19	AAW71363	Novel human diagno
594	6	2.8	247	20	AAW00640	Human fibroblast g	667	6	2.8	280	19	AAW71363	Novel human diagno
595	6	2.8	247	22	AAW31793	Human fibroblast g	668	6	2.8	280	19	AAW71363	Novel human diagno
						Propionibacterium				280	21	AAW71363	HIV POL/NEF epitop
										280	21	AAW71363	HIV POL/NEF epitop
										280	21	AAW71363	Eucalyptus grandis

669	280	2.8	6	Novel human diagno	742	6	2.8	345	21	AAB56897	Human prostate can
670	280	2.8	6	Synthetic HIV-deri	743	6	2.8	345	22	AAH83220	C. elegans FATPa si
671	280	2.8	6	Mycobacterium tube	744	6	2.8	347	19	AAW37743	S. pneumoniae DDL
672	281	2.8	6	Mouse ST-S1, used	745	6	2.8	347	22	AAH75610	Human colon cancer
673	282	2.8	6	Human ST-S1, used	746	6	2.8	348	22	AAH75207	Drosophila gustato
674	282	2.8	6	Human protein HP03	747	6	2.8	349	21	AAH85691	Murine Sam68-like
675	283	2.8	6	Novel human diagno	748	6	2.8	349	22	AAU00912	Staphylococcus hae
676	284	2.8	6	Novel human diagno	749	6	2.8	349	22	AAU09332	Murine SLM-1 prote
677	284	2.8	6	Human BCA-D5, Hom	750	6	2.8	350	19	AAW56265	Mouse recombinase
678	284	2.8	6	Arabidopsis thalia	751	6	2.8	350	21	AAH91933	Murine Rec2 serine
679	285	2.8	6	Arabidopsis thalia	752	6	2.8	353	8	AAH70407	ORF 4 gene product
680	285	2.8	6	Human protein sequ	753	6	2.8	353	18	AAW34338	Bean golden mosaic
681	286	2.8	6	Arabidopsis thalia	754	6	2.8	353	18	AAW34332	Bean golden mosaic
682	286	2.8	6	Arabidopsis thalia	755	6	2.8	353	18	AAW34333	Bean golden mosaic
683	288	2.8	6	Arabidopsis thalia	756	6	2.8	353	18	AAW34334	Bean golden mosaic
684	288	2.8	6	Propionibacterium	757	6	2.8	354	22	AAH34335	Novel human diagno
685	288	2.8	6	A representative H	758	6	2.8	354	22	AAH23844	Amino acid sequenc
686	288	2.8	6	A representative H	759	6	2.8	356	22	AAH18687	Tomato yellow leaf
687	302	2.8	6	Novel human diagno	760	6	2.8	357	18	AAW34337	Tomato yellow leaf
688	302	2.8	6	Novel human diagno	761	6	2.8	357	18	AAW34330	Tomato yellow leaf
689	302	2.8	6	Amino acid sequenc	762	6	2.8	357	18	AAW34331	Tomato yellow leaf
690	303	2.8	6	Burkholderia strai	763	6	2.8	357	18	AAW34331	Human protein sequ
691	303	2.8	6	Arabidopsis thalia	764	6	2.8	357	22	AAH94073	Human cytokine ras
692	304	2.8	6	Arabidopsis thalia	765	6	2.8	358	18	AAW08135	Human hp4 prostagl
693	304	2.8	6	Arabidopsis thalia	766	6	2.8	358	19	AAW44246	Human CR3 protei
694	304	2.8	6	Arabidopsis thalia	767	6	2.8	358	21	AAH87954	Human CR3 protei
695	306	2.8	6	Hydrophobic domain	768	6	2.8	358	22	AAH56383	Non-endogenous hum
696	308	2.8	6	Arabidopsis thalia	769	6	2.8	359	17	AAH88870	Sardinian tomato y
697	308	2.8	6	Chlamydia trachoma	770	6	2.8	359	17	AAH88871	Sardinian tomato y
698	309	2.8	6	Novel human diagno	771	6	2.8	359	17	AAH88872	Sardinian tomato y
699	309	2.8	6	C glutamicum prote	772	6	2.8	360	21	AAH70734	Human Wnt-2 protei
700	310	2.8	6	S. epidermidis ope	773	6	2.8	360	21	AAH57595	Human Wnt-2 protei
701	311	2.8	6	Arabidopsis thalia	774	6	2.8	360	22	AAH69160	Drosophila melanog
702	312	2.8	6	Arabidopsis thalia	775	6	2.8	361	8	AAH70562	Product of ORF 4 f
703	312	2.8	6	E. coli cellular p	776	6	2.8	361	18	AAW34336	Tomato mottle viru
704	313	2.8	6	Drosophila melanog	777	6	2.8	361	18	AAW34324	Tomato mottle viru
705	313	2.8	6	Haemophilus influe	778	6	2.8	361	18	AAW34325	Tomato mottle viru
706	313	2.8	6	Streptomyces plica	779	6	2.8	361	18	AAW34326	Tomato mottle viru
707	314	2.8	6	Arabidopsis thalia	780	6	2.8	362	22	AAU23384	Novel human enzyme
708	316	2.8	6	Propionibacterium	781	6	2.8	363	22	AAU17364	Novel signal trans
709	316	2.8	6	Human olfactory re	782	6	2.8	363	22	AAH81604	S. epidermidis ope
710	316	2.8	6	Human OR-like poly	783	6	2.8	364	17	AAH96031	P. gingivalis hagb
711	316	2.8	6	E6-binding protein	784	6	2.8	364	21	AAH69493	Protease protein h
712	317	2.8	6	Pseudomonas XpcX s	785	6	2.8	366	21	AAH49707	Arabidopsis thalia
713	317	2.8	6	Pseudomonas alcali	786	6	2.8	366	22	AAH25377	Arabidopsis thalia
714	317	2.8	6	Human olfactory re	787	6	2.8	369	22	AAU71877	C. glutamicum meta
715	317	2.8	6	Human olfactory re	788	6	2.8	369	22	AAH93194	C. glutamicum prote
716	317	2.8	6	Human OR-like poly	789	6	2.8	369	22	AAH79649	Corynebacterium gl
717	317	2.8	6	Pseudomonas alcali	790	6	2.8	369	22	AAH49698	Arabidopsis thalia
718	318	2.8	6	Human gene 8-encod	791	6	2.8	370	21	AAH49698	Arabidopsis thalia
719	321	2.8	6	Hepatitis C virus	792	6	2.8	371	21	AAH25376	Lignin peroxidase
720	321	2.8	6	Arabidopsis thalia	793	6	2.8	372	14	AAH42891	Arabidopsis thalia
721	322	2.8	6	Propionibacterium	794	6	2.8	372	14	AAH42891	Arabidopsis thalia
722	323	2.8	6	Human ORF3055	795	6	2.8	372	22	AAH65530	Drosophila melanog
723	323	2.8	6	Salmonella typhi c	796	6	2.8	372	22	AAH65530	Protein encoded by
724	323	2.8	6	Human olfactory re	797	6	2.8	373	21	AAH49706	Arabidopsis thalia
725	323	2.8	6	Human OR-like poly	798	6	2.8	373	21	AAH49706	Propionibacterium
726	323	2.8	6	Megamycin biosyn	799	6	2.8	376	22	AAU41830	Arabidopsis thalia
727	323	2.8	6	Drosophila melanog	800	6	2.8	378	21	AAH25795	Arabidopsis thalia
728	324	2.8	6	Amino acid sequenc	801	6	2.8	378	22	AAH25795	Novel human diagno
729	324	2.8	6	S. epidermidis ope	802	6	2.8	379	22	AAH49696	Arabidopsis thalia
730	324	2.8	6	A representative L	803	6	2.8	379	22	AAH11507	Novel human diagno
731	324	2.8	6	Amino acid sequenc	804	6	2.8	381	22	AAH66817	Drosophila melanog
732	326	2.8	6	Amino acid sequenc	805	6	2.8	381	22	AAH31613	Arabidopsis thalia
733	326	2.8	6	Human secreted pro	806	6	2.8	382	22	AAH20080	Novel human diagno
734	326	2.8	6	Human ORF3055	807	6	2.8	383	22	AAH20080	Novel human diagno
735	326	2.8	6	Novel human diagno	808	6	2.8	383	22	AAH10615	Human novel trypsi
736	326	2.8	6	Novel human diagno	809	6	2.8	383	22	AAH10615	Staphylococcus aur
737	326	2.8	6	Novel human diagno	810	6	2.8	388	22	AAH33916	Arabidopsis thalia
738	327	2.8	6	Salmonella typhi c	811	6	2.8	389	21	AAH33916	Arabidopsis thalia
739	327	2.8	6	Novel human diagno	812	6	2.8	389	21	AAH33916	Human hydrophobic
740	341	2.8	6	Putative P. abyss	813	6	2.8	390	22	AAH88577	Staphylococcus aur
741	342	2.8	6		814	6	2.8	391	21	AAH37011	Neisseria meningit

815	6	2.8	392	22	ABG06587	Novel human diagno	888	6	2.8	485	20	AAV34696	Chlamydia pneumoni
816	6	2.8	394	19	AAW69713	Streptomyces clavu	889	6	2.8	495	22	ABG01323	Novel human diagno
817	6	2.8	397	21	AAW43211	Human ORFX ORF2975	890	6	2.8	496	22	AAE1599	Streptococcus pneu
818	6	2.8	397	22	AAW90285	C glutamicum prote	891	6	2.8	497	21	AAE10616	Human novel trypsi
819	6	2.8	398	21	AAW93307	Human IGFAM-19 imm	892	6	2.8	497	22	AAW74446	Human protease-inh
820	6	2.8	398	22	ABW58306	Drosophila melanog	893	6	2.8	498	22	AAE10618	Human novel trypsi
821	6	2.8	400	16	AAW75203	Tyrosine phosphata	894	6	2.8	499	22	AAW93861	Human protein sequ
822	6	2.8	400	22	AAW42064	Human polypeptide	895	6	2.8	501	22	AAE10619	Human novel trypsi
823	6	2.8	401	12	AAW12130	ORF 2 of Igg light	896	6	2.8	504	21	AAW1574	Streptococcus pneu
824	6	2.8	401	22	AAW71917	C. glutamicum meta	897	6	2.8	505	22	AAW1574	Streptococcus pneu
825	6	2.8	401	22	ABG15468	Novel human diagno	898	6	2.8	506	21	AAW1574	Streptococcus pneu
826	6	2.8	401	22	AAW92077	C glutamicum prote	899	6	2.8	506	22	AAW1574	Streptococcus pneu
827	6	2.8	401	22	AAW97949	Corynebacterium gl	900	6	2.8	508	22	AAW49979	Drosophila melanog
828	6	2.8	401	22	AAW79993	Corynebacterium gl	901	6	2.8	508	22	AAW49979	Drosophila melanog
829	6	2.8	401	22	AAW80014	Corynebacterium gl	902	6	2.8	508	22	AAW49979	Drosophila melanog
830	6	2.8	407	22	ABG29590	Novel human diagno	903	6	2.8	509	18	AAW20085	Propionibacterium
831	6	2.8	409	21	AAW43705	Novel human diagno	904	6	2.8	514	22	AAE00224	Amino acid sequenc
832	6	2.8	411	20	AAW02353	Arabidopsis thalia	905	6	2.8	514	22	AAE00224	Helicobacter pylor
833	6	2.8	411	22	AAW63235	A representative L	906	6	2.8	517	22	ABG48240	Sus scrofa Prkag3
834	6	2.8	413	20	AAW02355	Amino acid sequenc	907	6	2.8	517	22	ABG02096	Amino acid sequenc
835	6	2.8	413	22	AAW63237	A representative L	908	6	2.8	521	22	AAU27781	Novel human diagno
836	6	2.8	415	19	AAW69228	Amino acid sequenc	909	6	2.8	521	22	AAU27781	Human full-length
837	6	2.8	415	21	AAW43114	Human lysosomal si	910	6	2.8	521	22	AAU23106	Novel human enzyme
838	6	2.8	415	21	AAW43114	Human ORFX ORF2878	911	6	2.8	522	21	AAW23661	Novel human enzyme
839	6	2.8	415	21	AAW85276	Arabidopsis thalia	912	6	2.8	523	21	AAW53796	Arabidopsis thalia
840	6	2.8	415	22	ABW68007	C. albicans Cair10	913	6	2.8	525	20	AAW72229	HSV-2 strain SB5 C
841	6	2.8	415	22	AAW67674	Drosophila melanog	914	6	2.8	525	20	AAW72229	Human secreted pro
842	6	2.8	418	22	AAU35812	Corynebacterium gl	915	6	2.8	527	19	AAW75776	Mycobacterium tube
843	6	2.8	418	22	ABG03314	Helicobacter pylor	916	6	2.8	527	19	AAW75776	Mycobacterium tube
844	6	2.8	419	18	AAW26465	Novel human diagno	917	6	2.8	534	21	AAW48359	Myobacterium bovi
845	6	2.8	419	22	AAW81240	Mycobacterial sery	918	6	2.8	534	22	ABG01344	Arabidopsis thalia
846	6	2.8	421	22	ABG20221	Novel human diagno	919	6	2.8	535	20	AAW59524	Novel human diagno
847	6	2.8	424	22	ABW60996	Drosophila melanog	920	6	2.8	535	20	AAU37783	Chlamydia trachoma
848	6	2.8	425	22	ABW68588	Drosophila melanog	921	6	2.8	536	22	AAU37783	Drosophila melanog
849	6	2.8	426	18	AAW20811	H. pylori inner me	922	6	2.8	536	22	AAU37783	Streptococcus pneu
850	6	2.8	426	21	AAW53602	Arabidopsis thalia	923	6	2.8	542	21	AAW73937	Human prostate tum
851	6	2.8	436	17	AAW03662	Human 70K UI snRNP	924	6	2.8	542	22	AAW73937	Arabidopsis thalia
852	6	2.8	436	20	AAW22342	70K UI snRNA bindi	925	6	2.8	550	21	AAW63703	Human protein sequ
853	6	2.8	440	21	AAW31611	Human prostate can	926	6	2.8	550	21	AAW63703	Human protein sequ
854	6	2.8	442	21	AAW56372	Arabidopsis thalia	927	6	2.8	557	22	AAW63703	Human protein sequ
855	6	2.8	442	21	AAW56372	Human prostate can	928	6	2.8	557	22	AAW63703	Human protein sequ
856	6	2.8	443	22	AAU30139	Novel human secret	929	6	2.8	560	22	ABG14573	Novel human diagno
857	6	2.8	445	22	ABW61688	Drosophila melanog	930	6	2.8	567	21	AAH03082	Human plant homeod
858	6	2.8	446	21	AAW53797	Arabidopsis thalia	931	6	2.8	567	22	AAU28257	Novel human secret
859	6	2.8	447	22	AAW72391	Barley LHT1 encode	932	6	2.8	571	22	ABG14031	Novel human diagno
860	6	2.8	449	22	AAW68879	Human RECAP polype	933	6	2.8	573	20	AAW04955	Mycobacterium spec
861	6	2.8	450	19	AAW46606	Tyrosine kinase as	934	6	2.8	574	21	AAW27327	A. thaliana NIM1 h
862	6	2.8	450	20	AAW29635	Human tyrosine kin	935	6	2.8	580	18	AAW25670	hNET sequence enco
863	6	2.8	450	20	AAW22130	Human tyrosine kin	936	6	2.8	580	19	AAW46758	Amino acid sequenc
864	6	2.8	450	22	ABG21667	Novel human diagno	937	6	2.8	583	22	ABG03333	Netrin protein seq
865	6	2.8	452	22	AAW70913	S cerevisiae apopt	938	6	2.8	584	22	ABG21351	Novel human diagno
866	6	2.8	453	21	AAW94340	Human cell surface	939	6	2.8	585	21	AAW49311	Novel human diagno
867	6	2.8	453	22	AAW91881	C glutamicum prote	940	6	2.8	585	22	AAW49311	Arabidopsis thalia
868	6	2.8	457	22	ABG11888	Novel human diagno	941	6	2.8	589	22	AAE01924	Arabidopsis thalia
869	6	2.8	458	22	AAU18482	Human endocrine po	942	6	2.8	591	20	AAW55964	Full length human
870	6	2.8	459	22	ABG29005	Novel human diagno	943	6	2.8	591	21	AAW55964	Human serine/threo
871	6	2.8	459	22	ABG29867	Novel human diagno	944	6	2.8	593	18	AAW20918	H. pylori transpor
872	6	2.8	462	12	AAW12401	Enantioselective a	945	6	2.8	594	22	ABW60224	Drosophila melanog
873	6	2.8	462	13	AAW25320	Enantioselective a	946	6	2.8	595	21	AAW52370	Escherichia coli F
874	6	2.8	464	22	AAE00222	Pig AMPK gamma sub	947	6	2.8	599	21	AAW21383	Arabidopsis thalia
875	6	2.8	466	19	AAW72230	HSV-2 strain SB5 C	948	6	2.8	599	22	AAW31083	Arabidopsis thalia
876	6	2.8	466	22	ABW70578	Drosophila melanog	949	6	2.8	601	22	AAW39498	Human polypeptide
877	6	2.8	468	20	AAW29114	Amino acid sequenc	950	6	2.8	605	22	AAW27306	Human protein prote
878	6	2.8	468	22	ABG14317	Novel human diagno	951	6	2.8	607	21	AAW81783	Human tyrosine phosp
879	6	2.8	470	22	ABW58174	Propionibacterium	952	6	2.8	607	21	AAW56098	Propionibacterium
880	6	2.8	471	22	AAW49242	S. pneumoniae hydr	953	6	2.8	608	22	AAW42195	Fusion protein con
881	6	2.8	477	19	AAW80695	Drosophila melanog	954	6	2.8	609	20	AAW41279	HSV-2 strain SB5 C
882	6	2.8	479	22	ABW62334	Novel human diagno	955	6	2.8	610	19	AAW72228	Arabidopsis thalia
883	6	2.8	482	22	AAW24912	Human novel cytoki	956	6	2.8	610	22	ABG28986	Novel human diagno
884	6	2.8	484	22	AAW68515	C glutamicum prote	957	6	2.8	610	22	ABG28986	Novel human diagno
885	6	2.8	484	22	AAW92676	Corynebacterium gl	958	6	2.8	613	21	AAW42369	Human ORFX ORF2133
886	6	2.8	484	22	AAW92676	Arabidopsis thalia	959	6	2.8	614	16	AAW82630	70K autoantigen, p
887	6	2.8	485	21	AAW44741		960	6	2.8	615	20	AAW14963	Amino acid sequenc

961	6	2.8	615	22	AAM79654	Human protein SEQ
962	6	2.8	616	22	AAM41284	Human polypeptide
963	6	2.8	617	20	AAV35424	Amino acid sequenc
964	6	2.8	618	13	AAR29928	Eimeria antigen Ea
965	6	2.8	619	19	AAW58566	Eimeria acervulina
966	6	2.8	620	22	ABG19308	Novel human diagno
967	6	2.8	622	22	AAM78670	Human protein SEQ
968	6	2.8	625	21	AAV92331	Human Trk oncogene
969	6	2.8	626	21	AAV88485	DraIII methylase D
970	6	2.8	627	22	AAU51580	Propionibacterium
971	6	2.8	628	21	AAG44740	Arabidopsis thalia
972	6	2.8	629	21	AAG48916	Arabidopsis thalia
973	6	2.8	631	22	AAU15923	Human novel secret
974	6	2.8	632	21	AAB26946	Wheat auxin transp
975	6	2.8	632	22	AAM40047	Human polypeptide
976	6	2.8	635	16	AAV74633	Nr (never ripe) to
977	6	2.8	635	16	AAR74629	Tomato ethylene re
978	6	2.8	635	19	AAW73125	Tomato ethylene re
979	6	2.8	635	19	AAW73124	Tomato ethylene re
980	6	2.8	636	20	AAW99183	Rhodococcus corall
981	6	2.8	637	18	AAW36182	Monkey p53 tumour
982	6	2.8	637	21	AAV97052	Rhodococcus sp. oh
983	6	2.8	639	21	AAG48915	Arabidopsis thalia
984	6	2.8	645	21	AAG21382	Arabidopsis thalia
985	6	2.8	645	21	AAG48914	Arabidopsis thalia
986	6	2.8	646	21	AAG31082	Arabidopsis thalia
987	6	2.8	646	22	ABB64598	Drosophila melanog
988	6	2.8	647	22	AAM23746	Human EST encoded
989	6	2.8	647	22	AAU14379	Human novel protei
990	6	2.8	649	19	AAW72097	HSV-2 strain S85 C
991	6	2.8	650	20	AAV14962	Amino acid sequenc
992	6	2.8	650	22	AAB83262	C elegans FATPa SE
993	6	2.8	650	22	AAB83274	C elegans FATPa SE
994	6	2.8	652	15	AAAB3808	Human amphotropic
995	6	2.8	652	19	AAW70499	Human sodium-lithi
996	6	2.8	655	22	AAB83263	C elegans FATPB SE
997	6	2.8	660	16	AAAB69633	Human interleukin-
998	6	2.8	660	21	AAAB54249	Human pancreatic c
999	6	2.8	662	16	AAAB69632	Human interleukin-
1000	6	2.8	662	18	AAW12772	Human interleukin-

ALIGNMENTS

RESULT 1
AAB18635
ID AAB18635 standard; Protein; 211 AA.
XX AAB18635;
DT 22-JAN-2001 (first entry)
XX
DE Amino acid sequence of human fibroblast growth factor (FGF)-20.
XX
KW p10-VEGFuc; gene delivery vector; eye disease; neovascular disease;
KW neurotrophic factor; anti-angiogenic factor; eye disease; glaucoma;
KW macular degeneration; diabetic retinopathy; retinitis pigmentosa;
KW inherited retinal degeneration; surgery-induced retinopathy;
KW retinal detachment; photic retinopathy; toxic retinopathy;
KW trauma-induced retinopathy; wet age related macular degeneration;
KW ARMD; retinopathy; fibroblast growth factor-20; FGF-20.
XX
OS Homo sapiens.
XX
XX WO200054813-A2.
PN 2000054813-A2.
XX
XX 21-SEP-2000.
PD
XX
XX 15-MAR-2000; 2000WO-US07062.
PF
XX
XX 15-MAR-1999; 99US-0124460.
PR
XX 06-JAN-2000; 2000US-0174984.

XX	(CHIR) CHIRON CORP.
PA	(REGC) UNIV CALIFORNIA.
PA	Manning WC, Dwarki VJ, Rendahl K, Zhou S, McGee LH, Lau D;
XX	Flannery JG, Miller S, Wang F, Di Polo A;
PI	WPI; 2000-618862/59.
PI	N-PSDB; AAA75630.
DR	Treating or preventing eye diseases or inhibiting neovascular disease
DR	of the eye, comprises intraocularly administering a gene delivery
XX	vector that directs expression of neurotrophic factors or
XX	anti-angiogenic factors -
PT	Disclosure; Fig 29; 86pp; English.
PS	The present sequence represents human fibroblast growth factor (FGF)-20.
XX	FGF-20 is expressed using a gene delivery vector of the invention.
CC	Vectors of the invention are used for treating or preventing eye
CC	diseases, or inhibiting neovascular disease of the eye. The gene
CC	delivery vector directs the expression of one or more neurotrophic
CC	factors, or anti-angiogenic factors, such that the disease of the eye
CC	is prevented or treated. The gene delivery vectors are useful for
CC	treating or preventing diseases of the eye such as macular degeneration,
CC	diabetic retinopathy, inherited retinal degeneration such as retinitis
CC	pigmentosa, glaucoma, surgery-induced retinopathy, retinal detachment,
CC	photic retinopathy, toxic retinopathy or trauma-induced retinopathy and
CC	for inhibiting neovascular diseases such as wet age related macular
CC	degeneration (ARMD) or retinopathy of prematurity.
XX	Sequence 211 AA;
SQ	Query Match 100.0%; Score 211; DB 21; Length 211;
	Best Local Similarity 100.0%; Pred. No. 1.1e-202;
	Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MAPLAEVGGFTGLGGLGQQVGSFLLPPAGERPPLGERSAERSARGGPGAQIAHL 60
Db	1 MAPLAEVGGFTGLGGLGQQVGSFLLPPAGERPPLGERSAERSARGGPGAQIAHL 60
Qy	61 HGILRRRLCYRTGPHQLIPDGSVQGTRODHSFLGILEFTSVAAGLVSRGVSGLYLG 120
Db	61 HGILRRRLCYRTGPHQLIPDGSVQGTRODHSFLGILEFTSVAAGLVSRGVSGLYLG 120
Qy	121 MNDKGLYSGEKLTSCEIFRQGFENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDCA 180
Db	121 MNDKGLYSGEKLTSCEIFRQGFENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDCA 180
Qy	181 SKRHOKFTHFLPRVPDPERVPELYKDLLMYT 211
Db	181 SKRHOKFTHFLPRVPDPERVPELYKDLLMYT 211
RESULT 2	
AAU09931	ID AAU09931 standard; Protein; 211 AA.
XX	AC AAU09931;
XX	DT 15-JAN-2002 (first entry)
XX	DE Human fibroblast growth factor-like (FGF-L) polypeptide sequence.
XX	Human; fibroblast growth factor-like; FGF-L; agonist; antagonist;
KW	vulnerable; virucide; hepatotropic; antiinflammatory; gut disorder;
KW	hepatitis; diabetes; wound healing; ulcer; liver disorder;
KW	lung disorder; angiogenesis.
XX	OS Homo sapiens.
XX	XX WO200168854-A2.
PN	
XX	

PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US08013.
XX
PR 13-MAR-2000; 2000US-188786P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Jing S, Bass MB;
XX
XX WPI; 2001-596910/67.
DR N-PSDB; AAS15701.
XX
XX New fibroblast growth factor-like polypeptide and polynucleotide for
PT diagnosis, prevention and treatment of diseases, disorders or
PT conditions involving the central nervous system, teeth, heart, liver or
PT adipose tissue -
XX
XX Claim 3; Fig 1; 116pp; English.
PS
XX
XX The present invention relates to new isolated fibroblast growth
CC factor-like (FGF-L) nucleic acid molecules and polypeptides. The FGF-L
CC polypeptide is useful for determining whether a compound inhibits FGF-L
CC polypeptide, and also for identifying a compound that binds to the
CC polypeptide. The FGF-L polypeptides of the invention are useful for
CC treating, preventing or ameliorating a medical condition or an FGF-L
CC polypeptide-related disease, condition or disorder such as wound healing
CC disorders, ulcers, gut disorders, lung disorders, liver disorders such as
CC hepatitis and diabetes. The invention is also useful for diagnosing a
CC pathological condition or susceptibility to a pathological condition in
CC a subject and is useful for modulating levels of FGF-L in an animal.
CC Other uses are detecting or quantifying the amount of FGF-L polypeptide
CC and for identifying or developing novel agonists and antagonists of the
CC FGF-L polypeptide signalling pathway which are useful for treating one
CC or more diseases or disorders, and also as an immunogen for producing
CC antibodies for in vivo imaging. The present sequence encodes the human
CC FGF-L polypeptide of the invention. The present sequence represents the
CC human FGF-L polypeptide of the invention.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 211; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.le-202;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQGVGSHFLPPAGERPPLLGERSAARSGGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQGVGSHFLPPAGERPPLLGERSAARSGGPGAAQLAHL 60
QY 61 HGILRRQLYCRGTFHQLQLPDGVSQGTQDHSFLGILEFISVAVGLVSIKGVDSGLYL 120
DB 61 HGILRRQLYCRGTFHQLQLPDGVSQGTQDHSFLGILEFISVAVGLVSIKGVDSGLYL 120
QY 121 MNDKGLYSGEKLTSCEIFREQEENWNTYSSNIYKHGDTGRRYFVALNKDGTGPRDGR 180
DB 121 MNDKGLYSGEKLTSCEIFREQEENWNTYSSNIYKHGDTGRRYFVALNKDGTGPRDGR 180
QY 181 SKRHQKTFHFLPRPVDPERVPELYKDLLMYT 211
DB 181 SKRHQKTFHFLPRPVDPERVPELYKDLLMYT 211
RESULT 3
AAG65666
ID AAG65666 standard; protein; 211 AA.
XX
AC AAG65666;
XX
DT 07-JAN-2002 (first entry)
XX
XX Human fibroblast growth factor (FGF)-20.
DE Human fibroblast growth factor (FGF)-20.
XX Fibroblast growth factor; FGF; FGF-like polypeptide; mitogenic;
KW

KW fat deposition; vulnery; antiulcer; dermatological; anorectic;
KW antidiabetic; antiinflammatory; cytostatic; hepatic; virucide;
XX neuroprotectant; pulmonary; gene therapy; vaccine; human.
OS Homo sapiens.
XX
PN WO200172957-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-IB00664.
XX
PR 31-MAR-2000; 2000US-0540118.
XX
PA (ITOH/) ITOH N.
XX
PI Itoh N;
XX
XX WPI; 2001-611623/70.
XX
XX New human nucleic acid encoding fibroblast growth factor-like peptide,
PT useful for treatment and diagnosis of e.g. wounds and inflammatory
PT bowel disease -
XX
PS Disclosure; Fig 3; 172pp; English.
XX
XX The invention provides human nucleic acids encoding fibroblast growth
CC factor (FGF)-like peptide. The FGF-like polypeptides can be expressed by
CC standard recombinant methodology and are mitogenic for a wide range of
CC cells, inducing differentiation and proliferation, and inhibiting
CC deposition of fat. The FGF-like polypeptides, polynucleotides and
CC specific antibodies and modulators are useful for treating a very wide
CC range of diseases and conditions, e.g. wounds, ulcers, skin aging,
CC obesity, diabetes, alopecia, inflammatory bowel disease, emphysema, viral
CC hepatitis, multiple sclerosis, respiratory distress syndrome, tumors of
CC the eye, etc., also for maintaining organs before transplant and
CC supporting culture of primary cells and tissues. Sequences AAG65647-67
CC represent amino acid sequences of some members of the FGF family.
XX
SQ Sequence 211 AA;
Query Match 100.0%; Score 211; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.le-202;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQGVGSHFLPPAGERPPLLGERSAARSGGPGAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQGVGSHFLPPAGERPPLLGERSAARSGGPGAAQLAHL 60
QY 61 HGILRRQLYCRGTFHQLQLPDGVSQGTQDHSFLGILEFISVAVGLVSIKGVDSGLYL 120
DB 61 HGILRRQLYCRGTFHQLQLPDGVSQGTQDHSFLGILEFISVAVGLVSIKGVDSGLYL 120
QY 121 MNDKGLYSGEKLTSCEIFREQEENWNTYSSNIYKHGDTGRRYFVALNKDGTGPRDGR 180
DB 121 MNDKGLYSGEKLTSCEIFREQEENWNTYSSNIYKHGDTGRRYFVALNKDGTGPRDGR 180
QY 181 SKRHQKTFHFLPRPVDPERVPELYKDLLMYT 211
DB 181 SKRHQKTFHFLPRPVDPERVPELYKDLLMYT 211
RESULT 4
AAU02081
ID AAU02081 standard; Protein; 211 AA.
XX
AC AAU02081;
XX
DT 07-SEP-2001 (first entry)
XX
XX Human fibroblast growth factor 20, FGF-20.
DE Human fibroblast growth factor 20; FGF-20; Parkinson's disease;
XX
KW Human; fibroblast growth factor 20; FGF-20; Parkinson's disease;

KW substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen;
KW antibody; neuro-degenerative disease; tendonitis; wound healing;
KW stroke; ischaemia.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Binding-site 170..186
FT /label= Heparin_binding_site
XX
XX WO200131008-A2.
XX
XX 03-MAY-2001.
XX
XX 20-OCT-2000; 2000WO-US29237.
XX
XX 22-OCT-1999; 99US-0161162.
PR 08-MAR-2000; 2000US-0187836.
XX
XX (CHIR) CHIRON CORP.
PA (KYOG) UNIV KYOTO.
XX
XX Itoh N, Kavanaugh WM;
XX
XX WPI: 2001-308642/32.
DR N-PSDB; AAS03277.
XX
XX New human and rat Fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions -
XX
XX Claim 12; Fig 8; 73pp; English.
XX
XX The sequence is Human fibroblast growth factor 20, FGF-20. The FGF
CC polypeptides and nucleic acids encoding them are useful for providing
CC trophic support for cells in a patient, especially a patient with
CC Parkinson's disease, and FGF-20 is additionally used to treat patients
CC with conditions of the substantia nigra. The polypeptides and nucleic
CC acids are useful for alleviating human brain conditions by slowing
CC degeneration, restoring function of, or increasing the number of,
CC dopaminergic neurons. The polypeptides and nucleic acids are also
CC useful for alleviating cochlea-associated disease by slowing
CC degeneration of or restoring or maintaining normal function of the
CC structure of cochlea, where the disease is otosclerosis, Cogan's
CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
CC hearing loss, congenital malformations, autoimmune disease-related
CC hearing loss, age-related hearing loss, deafness associated with lack
CC of FGF receptor and ischaemia-related hearing disturbance. Other
CC diseases thought to be amenable to FGF therapeutic activity include
CC neuro-degenerative diseases, tendonitis, wound healing, stroke and
CC ischaemia. The polypeptides can be used to screen for agonists and
CC antagonists. Epitope bearing fragments of the FGF-20 polypeptides can be
CC used to raise anti-FGF-20 antibodies.
XX
XX Sequence 211 AA;
SQ
Query Match 100.0%; Score 211; DB 22; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.1e-202;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGGLGQQVGSFLPPAGERPPLLGERRSAERSARGGPCAAQLAHL 60
DB 1 MAPLAEVGGFLGGLGQQVGSFLPPAGERPPLLGERRSAERSARGGPCAAQLAHL 60
QY 61 HGILRRRLQYCRGTGPHLQILPDGSGVQGTQDHSFLGILEFISVAVGLVSRGVDSGLYIG 120
DB 61 HGILRRRLQYCRGTGPHLQILPDGSGVQGTQDHSFLGILEFISVAVGLVSRGVDSGLYIG 120
QY 121 MNDKGLYSGSEKLTSECIFREQFENWNTYSSNIYKHGDTGRRYFVALNKDGTDRDGR 180

DB 121 MNDKGLYSGSEKLTSECIFREQFENWNTYSSNIYKHGDTGRRYFVALNKDGTDRDGR 180
QY 181 SKRHQKFTFLPRPDPVDPERVPPELYKDLLMYT 211
DB 181 SKRHQKFTFLPRPDPVDPERVPPELYKDLLMYT 211
RESULT 5
AAB62817
ID AAB62817 standard; Protein; 211 AA.
XX
XX AAB62817;
AC
XX
XX 02-MAY-2001 (first entry)
XX
XX Human fibroblast growth factor-CX (FGF-CX) amino acid sequence.
XX
XX Fibroblast growth factor-CX; FGF-CX; wound healing; haematopoiesis;
KW cell growth; proliferation; tumour; restenosis; psoriasis; human;
KW Dupuytren's contracture; Kaposi sarcoma; rheumatoid arthritis;
KW cartilage repair; bone repair; exostosis; hallux valgus deformity;
KW achondroplasia; cerebral lesion; cerebral oedema; senile dementia;
KW Alzheimer's disease; diabetic neuropathy; osteoporosis.
XX
XX Homo sapiens.
XX
XX WO200107595-A2.
XX
XX 01-FEB-2001.
XX
XX 27-JUL-2000; 2000WO-US20405.
XX
XX 27-JUL-1999; 99US-0145899.
PR 31-JAN-2000; 2000US-0494585.
PR 03-JUL-2000; 2000US-0609543.
XX
XX {CURA-} CURAGEN CORP.
XX
XX Jeffers M, Shimkets RA, Prayaga SK, Boldog FL, Yang M, Burgess C;
PI Fernandes E, Herrmann JL, Larochele WJ, Lichenstein H;
PI
XX WPI: 2001-159717/16.
DR N-PSDB; AAF62049.
XX
XX New human fibroblast growth factor FGF-CX polypeptide, useful for
PT treating tissue proliferation disorders such as tumors, restenosis,
PT psoriasis, diabetic complications, Kaposi sarcoma and rheumatoid
PT arthritis -
XX
XX Claim 1; Fig 1; 128pp; English.
XX
XX This invention relates to human fibroblast growth factor-CX (FGF-CX) and
CC the DNA sequence encoding it. FGF-CX protein and polynucleotide sequences
CC are useful for treating or preventing a disorder associated with aberrant
CC expression, processing or physiological interactions of FGF-CX
CC characterised by insufficient or ineffective growth of a cell or tissue.
CC FGF-CX is also useful for promoting growth of cells which are in the
CC vicinity of a wound, vascular system, those involved in haematopoiesis or
CC erythropoiesis, cells in the lining of the gastrointestinal tract or
CC cells in hair follicles. Other uses include, inhibiting cell growth.
CC FGF-CX is useful for treating, preventing or delaying a tissue
CC proliferative disorder such as tumours, restenosis, psoriasis,
CC Dupuytren's contracture, diabetic complications, Kaposi sarcoma, and
CC rheumatoid arthritis. Compositions containing FGF-CX can be used to
CC stimulate cartilage or bone repair. Compositions containing FGF-CX
CC binding agents can be used to treat diseases such as multiple or solitary
CC hereditary exostosis, hallux valgus deformity and achondroplasia. FGF-CX
CC may be used in diagnosing or treating glial cell related disorders,
CC cerebral lesions or to treat cerebral oedema, senile dementia,
CC Alzheimer's disease, or diabetic neuropathy. FGF-CX also has
CC osteogenesis-promoting activity and can be used for treating bone
CC fractures and osteoporosis. FGF-CX polypeptides may be used as platelet


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CC increasing agents, or for treating cerebral nervous diseases. The present
CC sequence represents the human FGF-CX protein.
XX
SQ Sequence 211 AA;
  Query Match 100.0%; Score 211; DB 22; Length 211;
  Best Local Similarity 100.0%; Pred. No. 1.1e-202;
  Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEVGGFLGLEGQQGVSHFLPPAGERPPLGERSAAERSARGGPAQAHL 60
DB 1 MAPLAEVGGFLGLEGQQGVSHFLPPAGERPPLGERSAAERSARGGPAQAHL 60
QY 61 HGILRRQLYCRFTGFLQILPDGVSQGTQDHSFLGILFISVAVGLSVIRGVDGSLYL 120
DB 61 HGILRRQLYCRFTGFLQILPDGVSQGTQDHSFLGILFISVAVGLSVIRGVDGSLYL 120
QY 121 MNDKGYLGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGR 180
DB 121 MNDKGYLGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGR 180
QY 181 SKRHKQFTFLPRPDPVPELYKDLLMYT 211
DB 181 SKRHKQFTFLPRPDPVPELYKDLLMYT 211
RESULT 6
AAU02080
ID AAU02080 standard; Protein; 212 AA.
XX
AC AAU02080;
XX
DT 07-SEP-2001 (first entry)
XX
DE Rat fibroblast growth factor 20, FGF-20.
XX
KW Rat; fibroblast growth factor 20; FGF-20; Parkinson's disease;
KW substantia nigra; dopaminergic neuron; cochlea-associated disease;
KW otosclerosis; Cogan's syndrome; Meniere's disease; Pendred's syndrome;
KW diabetes-associated hearing loss; congenital malformations;
KW autoimmune disease-related hearing loss; age-related hearing loss;
KW deafness; ischaemia-related hearing disturbance; immunogen;
KW antibody; neuro-degenerative disease; tendonitis; wound healing;
KW stroke; ischaemia.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Peptide 56..70
FT /label= Epitope
FT /note= "Peptide used to raise anti-FGF-20 antibodies"
FT Binding-site 170..186
FT /label= Heparin_binding_site
FT Peptide 176..189
FT /label= Epitope
FT /note= "Peptide used to raise anti-FGF-20 antibodies"
XX
PN WO200131008-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US29237.
XX
PR 22-OCT-1999; 99US-0161162.
PR 08-MAR-2000; 2000US-0187856.
XX
XX (CHIR ) CHIRON CORP.
PA (YTOU ) UNIV KYOTO.
XX
XX Itoh N, Kavanaugh WM;
XX
XX WPI: 2001-308642/32.
XX
XX N-PSDB; AAS03276.
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XX New human and rat Fibroblast Growth Factor (FGF) polypeptides for
PT providing trophic support for cells used in Parkinson patients, and
PT alleviating brain and cochlea conditions -
XX
XX Claim 45; Fig 7; 73pp; English.
XX
CC The sequence is Rat fibroblast growth factor 20, FGF-20. The FGF
CC polypeptides and nucleic acids encoding them are useful for providing
CC trophic support for cells in a patient, especially a patient with
CC Parkinson's disease, and FGF-20 is additionally used to treat patients
CC with conditions of the substantia nigra. The polypeptides and nucleic
CC acids are useful for alleviating human brain conditions by slowing
CC degeneration, restoring function of, or increasing the number of,
CC dopaminergic neurons. The polypeptides and nucleic acids are also
CC useful for alleviating cochlea-associated disease by slowing of the
CC degeneration of or restoring or maintaining normal function of the
CC structure of cochlea, where the disease is otosclerosis, Cogan's
CC syndrome, Meniere's disease, Pendred's syndrome, diabetes-associated
CC hearing loss, congenital malformations, autoimmune disease-related
CC hearing loss, age-related hearing loss, deafness associated with lack
CC of FGF receptor and ischaemia-related hearing disturbance. Other
CC diseases thought to be amenable to FGF therapeutic activity include
CC neuro-degenerative diseases, tendonitis, wound healing, stroke and
CC ischaemia. The polypeptides can be used to screen for agonists and
CC antagonists. Epitope bearing fragments of the FGF-20 polypeptides can be
CC used to raise anti-FGF-20 antibodies.
XX
SQ Sequence 212 AA;
  Query Match 40.3%; Score 85; DB 22; Length 212;
  Best Local Similarity 100.0%; Pred. No. 1.1e-76;
  Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 KGELYGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGRSKR 183
DB 124 KGELYGSEKLTSECIFREQFEENWNTYSSNIYKHGDTGRYFVALNKDGTPRDGRSKR 183
QY 184 HKQFTFLPRPDPVPELYKDLL 208
DB 184 HKQFTFLPRPDPVPELYKDLL 208
RESULT 7
AAR56503
ID AAR56503 standard; peptide; 142 AA.
XX
AC AAR56503;
XX
DT 06-MAR-1995 (first entry)
XX
DE Glia activating factor (GAF) peptide.
XX
DE Glia activating factor; GAF; testing; detection; antibody; cancer;
KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.
XX
XX Homo sapiens.
XX
PN EP608546-A.
XX
PD 03-AUG-1994.
XX
PF 18-DEC-1993; 93EP-0120491.
XX
PR 22-DEC-1992; 92JP-0342100.
PR 23-AUG-1993; 93JP-0207719.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;
XX
XX WPI: 1994-242006/30.
XX
```

PT New glia activating factor polypeptide and antibodies - for use
 PT in detection, purification and treatment of diseases, e.g. as
 PT anticancer or platelet-increasing agents.

XX
 XX Disclosure; Page 38-39; 80pp; English.

CC The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
 CC be used as platelet increasing agents, osteogenesis promoting
 CC agents or for treating cerebral nervous diseases or hepatopathy such
 CC as hepatic cirrhosis. They can also be used to treat cancer when
 CC used alongside an anticancer agent. Antibodies directed against the
 CC GAF polypeptides can be used for detecting or determining a
 CC biological activity of a GAF polypeptide or for purifying a GAF
 CC polypeptide. The antibodies, which also neutralise the cell growth
 CC activity of GAF, can be used as anticancer agents.

XX
 XX Sequence 142 AA;

Query Match 9.0%; Score 19; DB 15; Length 142;

Best Local Similarity 100.0%; Pred. No. 7.5e-11; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;

Qy 104 AVGLVSIRGVDSGLYLGWN 122
 |||||

Db 48 AVGLVSIRGVDSGLYLGWN 66

RESULT 8

AAR56510

ID AAR56510 standard; peptide; 159 AA.

XX
 AC AAR56510;

XX
 DT 06-MAR-1995 (first entry)

XX
 DE Glia activating factor (GAF) peptide.

XX
 KW Glia activating factor; GAF; testing; detection; antibody; cancer;
 KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.

XX
 OS Homo sapiens.

XX
 PN EP608546-A.

XX
 PD 03-AUG-1994.

XX
 PF 18-DEC-1993; 93EP-0120491.

XX
 PR 22-DEC-1992; 92JP-0342100.

XX
 PR 23-AUG-1993; 93JP-0207719.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.

XX
 PI Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;

XX
 DR WPI; 1994-242006/30.

XX
 PT New glia activating factor polypeptide and antibodies - for use
 PT in detection, purification and treatment of diseases, e.g. as
 PT anticancer or platelet-increasing agents.

XX
 PS Disclosure; Page 45; 80pp; English.

XX The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
 CC be used as platelet increasing agents, osteogenesis promoting
 CC agents or for treating cerebral nervous diseases or hepatopathy such
 CC as hepatic cirrhosis. They can also be used to treat cancer when
 CC used alongside an anticancer agent. Antibodies directed against the
 CC GAF polypeptides can be used for detecting or determining a
 CC biological activity of a GAF polypeptide or for purifying a GAF
 CC polypeptide. The antibodies, which also neutralise the cell growth
 CC activity of GAF, can be used as anticancer agents.

XX

SQ Sequence 159 AA;

Query Match 9.0%; Score 19; DB 15; Length 159;

Best Local Similarity 100.0%; Pred. No. 8.3e-11; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;

Qy 104 AVGLVSIRGVDSGLYLGWN 122
 |||||

Db 52 AVGLVSIRGVDSGLYLGWN 70

RESULT 9

AAR56511

ID AAR56511 standard; peptide; 160 AA.

XX
 AC AAR56511;

XX
 DT 06-MAR-1995 (first entry)

XX
 DE Glia activating factor (GAF) peptide.

XX
 KW Glia activating factor; GAF; testing; detection; antibody; cancer;
 KW osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.

XX
 OS Homo sapiens.

XX
 PN EP608546-A.

XX
 PD 03-AUG-1994.

XX
 PF 18-DEC-1993; 93EP-0120491.

XX
 PR 22-DEC-1992; 92JP-0342100.

XX
 PR 23-AUG-1993; 93JP-0207719.

XX
 PA (TAKE) TAKEDA CHEM IND LTD.

XX
 PI Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;

XX
 DR WPI; 1994-242006/30.

XX
 PT New glia activating factor polypeptide and antibodies - for use
 PT in detection, purification and treatment of diseases, e.g. as
 PT anticancer or platelet-increasing agents.

XX
 PS Disclosure; Page 46; 80pp; English.

XX The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
 CC be used as platelet increasing agents, osteogenesis promoting
 CC agents or for treating cerebral nervous diseases or hepatopathy such
 CC as hepatic cirrhosis. They can also be used to treat cancer when
 CC used alongside an anticancer agent. Antibodies directed against the
 CC GAF polypeptides can be used for detecting or determining a
 CC biological activity of a GAF polypeptide or for purifying a GAF
 CC polypeptide. The antibodies, which also neutralise the cell growth
 CC activity of GAF, can be used as anticancer agents.

SQ Sequence 160 AA;

Query Match 9.0%; Score 19; DB 15; Length 160;

Best Local Similarity 100.0%; Pred. No. 8.3e-11; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0;

Qy 104 AVGLVSIRGVDSGLYLGWN 122
 |||||

Db 53 AVGLVSIRGVDSGLYLGWN 71

RESULT 10

AAR56508

ID AAR56508 standard; peptide; 175 AA.

XX
 AC AAR56508;

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XX 06-MAR-1995 (first entry)
XX Glia activating factor (GAF) peptide.
XX Glia activating factor; GAF; testing; detection; antibody; cancer;
XX osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.
XX Homo sapiens.
XX EP608546-A.
XX 03-AUG-1994.
XX 18-DEC-1993; 93EP-0120491.
XX 22-DEC-1992; 92JP-0342100.
XX 23-AUG-1993; 93JP-0207719.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;
XX WPI; 1994-242006/30.
XX New glia activating factor polypeptide and antibodies - for use
XX in detection, purification and treatment of diseases, e.g. as
XX anticancer or platelet-increasing agents.
XX Disclosure; Page 43-44; 80pp; English.
XX The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
XX be used as platelet increasing agents, osteogenesis promoting
XX agents or for treating cerebral nervous diseases or hepatopathy such
XX as hepatic cirrhosis. They can also be used to treat cancer when
XX used alongside an anticancer agent. Antibodies directed against the
XX GAF polypeptides can be used for detecting or determining a
XX biological activity of a GAF polypeptide or for purifying a GAF
XX polypeptide. The antibodies, which also neutralise the cell growth
XX activity of GAF, can be used as anticancer agents.
XX Sequence 175 AA;
XX Query Match 9.0%; Score 19; DB 15; Length 175;
XX Best Local Similarity 100.0%; Pred. No. 9e-11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 104 AVGLVSIKRGVDSGLYLGMN 122
XX |||||
XX 58 AVGLVSIKRGVDSGLYLGMN 86
XX |||||
XX
XX RESULT 11
XX AAR56509
XX ID AAR56509 standard; peptide; 176 AA.
XX AC AAR56509;
XX XX
XX 06-MAR-1995 (first entry)
XX Glia activating factor (GAF) peptide.
XX Glia activating factor; GAF; testing; detection; antibody; cancer;
XX osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.
XX Homo sapiens.
XX EP608546-A.
XX 03-AUG-1994.
XX 18-DEC-1993; 93EP-0120491.
XX
XX Query Match 9.0%; Score 19; DB 15; Length 175;
XX Best Local Similarity 100.0%; Pred. No. 9e-11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 104 AVGLVSIKRGVDSGLYLGMN 122
XX |||||
XX 58 AVGLVSIKRGVDSGLYLGMN 86
XX |||||
XX
XX RESULT 12
XX AAR27208
XX ID AAR27208 standard; Protein; 177 AA.
XX AC AAR27208;
XX XX
XX 20-MAY-1998 (first entry)
XX Glia activating factor #2.
XX GAF; stimulates glial cell growth; cerebral nerve cell lesions;
XX cerebral oedema; alzheimers disease; senile dementia;
XX diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
XX stimulates megakaryocytes; increase platelets; haematopoietic cells;
XX immunocompetent cells; vascular smooth muscle cells; bone fractures;
XX osteogenesis promoting activity; osteoporosis; cerebral tumours;
XX stimulates cultured cells.
XX Homo sapiens.
XX OS
XX XX
XX EP503297-A.
XX PN
XX XX
XX 16-SEP-1992.
XX PD
XX XX
XX 13-FEB-1992; 92EP-0102385.
XX PF
XX XX
XX 14-FEB-1991; 91JP-0020860.
XX PR
XX 04-SEP-1991; 91JP-0224454.
XX PR
XX 10-JAN-1992; 92JP-0003399.
XX PR
XX (TAKE ) TAKEDA CHEM IND LTD.
XX PA
XX Kondo T, Kurokawa T, Naruo K, Seko C;
XX PI
XX WPI; 1992-309482/38.
XX DR
XX N-PSDB; AAQ28411.
XX DR
XX

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PR 22-DEC-1992; 92JP-0342100.
XX 23-AUG-1993; 93JP-0207719.
XX (TAKE ) TAKEDA CHEM IND LTD.
XX Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;
XX WPI; 1994-242006/30.
XX New glia activating factor polypeptide and antibodies - for use
XX in detection, purification and treatment of diseases, e.g. as
XX anticancer or platelet-increasing agents.
XX Disclosure; Page 44; 80pp; English.
XX The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
XX be used as platelet increasing agents, osteogenesis promoting
XX agents or for treating cerebral nervous diseases or hepatopathy such
XX as hepatic cirrhosis. They can also be used to treat cancer when
XX used alongside an anticancer agent. Antibodies directed against the
XX GAF polypeptides can be used for detecting or determining a
XX biological activity of a GAF polypeptide or for purifying a GAF
XX polypeptide. The antibodies, which also neutralise the cell growth
XX activity of GAF, can be used as anticancer agents.
XX Sequence 176 AA;
XX Query Match 9.0%; Score 19; DB 15; Length 176;
XX Best Local Similarity 100.0%; Pred. No. 9e-11;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 104 AVGLVSIKRGVDSGLYLGMN 122
XX |||||
XX 69 AVGLVSIKRGVDSGLYLGMN 87
XX |||||
XX
XX RESULT 12
XX AAR27208
XX ID AAR27208 standard; Protein; 177 AA.
XX AC AAR27208;
XX XX
XX 20-MAY-1998 (first entry)
XX Glia activating factor #2.
XX GAF; stimulates glial cell growth; cerebral nerve cell lesions;
XX cerebral oedema; alzheimers disease; senile dementia;
XX diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
XX stimulates megakaryocytes; increase platelets; haematopoietic cells;
XX immunocompetent cells; vascular smooth muscle cells; bone fractures;
XX osteogenesis promoting activity; osteoporosis; cerebral tumours;
XX stimulates cultured cells.
XX Homo sapiens.
XX OS
XX XX
XX EP503297-A.
XX PN
XX XX
XX 16-SEP-1992.
XX PD
XX XX
XX 13-FEB-1992; 92EP-0102385.
XX PF
XX XX
XX 14-FEB-1991; 91JP-0020860.
XX PR
XX 04-SEP-1991; 91JP-0224454.
XX PR
XX 10-JAN-1992; 92JP-0003399.
XX PR
XX (TAKE ) TAKEDA CHEM IND LTD.
XX PA
XX Kondo T, Kurokawa T, Naruo K, Seko C;
XX PI
XX WPI; 1992-309482/38.
XX DR
XX N-PSDB; AAQ28411.
XX DR
XX

```

PT Glia activating factor and its DNA - specifically promotes growth
PT of glial cells, for treating e.g. cerebral lesions, Alzheimer's
PT disease, diabetic neuropathies, etc., also in diagnosis
XX PS Claim 1; Fig 19; 87pp; English.
XX This sequence represents a glia activating factor. It stimulates the
CC growth of glia cells and can be used to accelerate healing of cerebral
CC lesions or treat cerebral oedema, alzheimers disease, senile dementia,
CC or diabetic neuropathy. It also stimulates fibroblasts (for accelerating
CC healing of burns, wounds, ulcers, etc) megakaryocytes (to increase the
CC no. of platelets), haematopoietic, immunocompetent and vascular smooth
CC muscle cells. It is also expected to have osteogenesis-promoting activity
CC (for treating bone fractures and osteoporosis) Assay of this factor may
CC be useful in diagnosis of cerebral tumours, and antibodies against could
CC be used to treat such tumours. It can also be used as a reagent for
CC stimulating growth of cultured cells. Dosage is 1ng-0.1mg/kg/day.
XX SQ Sequence 177 AA;
Query Match 9.0%; Score 19; DB 13; Length 177;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 AVGLVSRGVDSGLYLGMN 122
|||||
DB 70 AVGLVSRGVDSGLYLGMN 88
|||||
RESULT 13
AAR27210
ID AAR27210 standard; Protein; 178 AA.
AC AAR27210;
XX 20-MAY-1998 (first entry)
XX Glia activating factor #4.
DE GAF; stimulates glial cell growth; cerebral nerve cell lesions;
KW cerebral oedema; alzheimers disease; senile dementia;
KW diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
KW stimulates megakaryocytes; increase platelets; haematopoietic cells;
KW immunocompetent cells; vascular smooth muscle cells; bone fractures;
KW osteogenesis promoting activity; osteoporosis; cerebral tumours;
KW stimulates cultured cells.
XX Homo sapiens.
OS
XX EP503297-A.
XX 16-SEP-1992.
XX 13-FEB-1992; 92EP-0102385.
XX 14-FEB-1991; 91JP-0020860.
XX 04-SEP-1991; 91JP-0224454.
XX 10-JAN-1992; 92JP-0003399.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Kondo T, Kurokawa T, Naruo K, Seko C;
XX WPI; 1992-309482/38.
XX Glia activating factor and its DNA - specifically promotes growth
PT of glial cells, for treating e.g. cerebral lesions, Alzheimer's
PT disease, diabetic neuropathies, etc., also in diagnosis
XX PS Claim 1; Pg5; 7pp; English.
XX This sequence represents a glia activating factor. It stimulates the
CC growth of glia cells and can be used to accelerate healing of cerebral

CC lesions or treat cerebral oedema, alzheimers disease, senile dementia,
CC or diabetic neuropathy. It also stimulates fibroblasts (for accelerating
CC healing of burns, wounds, ulcers, etc) megakaryocytes (to increase the
CC no. of platelets), haematopoietic, immunocompetent and vascular smooth
CC muscle cells. It is also expected to have osteogenesis-promoting activity
CC (for treating bone fractures and osteoporosis) Assay of this factor may
CC be useful in diagnosis of cerebral tumours, and antibodies against could
CC be used to treat such tumours. It can also be used as a reagent for
CC stimulating growth of cultured cells. Dosage is 1ng-0.1mg/kg/day.
XX SQ Sequence 178 AA;
Query Match 9.0%; Score 19; DB 13; Length 178;
Best Local Similarity 100.0%; Pred. No. 9.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 104 AVGLVSRGVDSGLYLGMN 122
|||||
DB 71 AVGLVSRGVDSGLYLGMN 89
|||||
RESULT 14
AAR27209
ID AAR27209 standard; Protein; 205 AA.
AC AAR27209;
XX 20-MAY-1998 (first entry)
XX Glia activating factor #3.
DE GAF; stimulates glial cell growth; cerebral nerve cell lesions;
KW cerebral oedema; alzheimers disease; senile dementia;
KW diabetic neuropathy; stimulates fibroblasts; burns; wounds; ulcers;
KW stimulates megakaryocytes; increase platelets; haematopoietic cells;
KW immunocompetent cells; vascular smooth muscle cells; bone fractures;
KW osteogenesis promoting activity; osteoporosis; cerebral tumours;
KW stimulates cultured cells.
XX Homo sapiens.
OS
XX EP503297-A.
XX 16-SEP-1992.
XX 13-FEB-1992; 92EP-0102385.
XX 14-FEB-1991; 91JP-0020860.
XX 04-SEP-1991; 91JP-0224454.
XX 10-JAN-1992; 92JP-0003399.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Kondo T, Kurokawa T, Naruo K, Seko C;
XX WPI; 1992-309482/38.
XX Glia activating factor and its DNA - specifically promotes growth
PT of glial cells, for treating e.g. cerebral lesions, Alzheimer's
PT disease, diabetic neuropathies, etc., also in diagnosis
XX PS Claim 1; Pg5; 7pp; English.
XX This sequence represents a glia activating factor. It stimulates the
CC growth of glia cells and can be used to accelerate healing of cerebral
CC lesions or treat cerebral oedema, alzheimers disease, senile dementia,
CC or diabetic neuropathy. It also stimulates fibroblasts (for accelerating
CC healing of burns, wounds, ulcers, etc) megakaryocytes (to increase the
CC no. of platelets), haematopoietic, immunocompetent and vascular smooth
CC muscle cells. It is also expected to have osteogenesis-promoting activity
CC (for treating bone fractures and osteoporosis) Assay of this factor may
CC be useful in diagnosis of cerebral tumours, and antibodies against could
CC be used to treat such tumours. It can also be used as a reagent for

CC stimulating growth of cultured cells. Dosage is lng-0.1mg/kg/day.

SQ Sequence 205 AA;

Query Match 9.0%; Score 19; DB 13; Length 205;

Best Local Similarity 100.0%; Pred. No. 1e-10;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 AVGLVSIRGVDSGLYLGMN 122

|||||

DB 98 AVGLVSIRGVDSGLYLGMN 116

RESULT 15

AAR56506

ID AAR56506 standard; peptide; 205 AA.

XX AC AAR56506;

XX DT 06-MAR-1995 (first entry)

XX DE Glia activating factor (GAF) peptide.

XX KW Glia activating factor; GAF; testing; detection; antibody; cancer;

XX OS osteogenesis; platelet; hepatopathy; cirrhosis; anticancer agent.

XX PN Homo sapiens.

XX PD EP608546-A.

XX PF 03-AUG-1994.

XX PR 18-DEC-1993; 93EP-0120491.

XX PR 22-DEC-1992; 92JP-0342100.

XX PR 23-AUG-1993; 93JP-0207719.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Kurokawa T, Kuroshima K, Seko C, Yoshitomi S;

XX DR WPI; 1994-242006/30.

XX PT New glia activating factor polypeptide and antibodies - for use

in detection, purification and treatment of diseases, e.g. as

anticancer or platelet-increasing agents.

XX PS Disclosure; Page 41-42; 80pp; English.

XX CC The glia activating factor (GAF) polypeptides (See AAR56503-56511) can
be used as platelet increasing agents, osteogenesis promoting
agents or for treating cerebral nervous diseases or hepatopathy such
as hepatic cirrhosis. They can also be used to treat cancer when
used alongside an anticancer agent. Antibodies directed against the
GAF polypeptides can be used for detecting or determining a
biological activity of a GAF polypeptide or for purifying a GAF
polypeptide. The antibodies, which also neutralise the cell growth
activity of GAF, can be used as anticancer agents.

SQ Sequence 205 AA;

Query Match

Best Local Similarity 9.0%; Score 19; DB 15; Length 205;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 104 AVGLVSIRGVDSGLYLGMN 122

|||||

DB 98 AVGLVSIRGVDSGLYLGMN 116

Search completed: October 21, 2002, 16:19:55

Job time : 70 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:18:46 ; Search time 13 Seconds
(without alignments)
396.446 Million cell updates/sec

Title: US-09-817-814-2
Perfect score: 211
Sequence: 1 MAPLAEVGFLGGLEGQQ.....PRVDPERVPELYKDLLMYT 211

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA:*
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2: /cgn2.6/ptodata/1/iaa/5B-COMB.pep:*
3: /cgn2.6/ptodata/1/iaa/6A-COMB.pep:*
4: /cgn2.6/ptodata/1/iaa/6B-COMB.pep:*
5: /cgn2.6/ptodata/1/iaa/PCTUS-COMB.pep:*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	9.0	142	1	US-08-340-820-1
2	19	9.0	142	1	US-08-172-328-1
3	19	9.0	142	1	US-08-593-535-1
4	19	9.0	159	1	US-08-172-328-8
5	19	9.0	160	1	US-08-172-328-9
6	19	9.0	175	1	US-08-172-328-6
7	19	9.0	176	1	US-08-172-328-7
8	19	9.0	177	1	US-08-340-820-4
9	19	9.0	177	1	US-08-593-535-4
10	19	9.0	178	1	US-08-340-820-6
11	19	9.0	178	1	US-08-441-629-16
12	19	9.0	190	1	US-08-776-207-16
13	19	9.0	190	3	PCT-US95-09172-16
14	19	9.0	193	2	US-08-438-439C-21
15	19	9.0	205	1	US-08-340-820-5
16	19	9.0	205	1	US-08-172-328-4
17	19	9.0	205	1	US-08-593-535-5
18	19	9.0	206	1	US-08-340-820-7
19	19	9.0	206	1	US-08-340-820-8
20	19	9.0	206	1	US-08-172-328-5
21	19	9.0	206	1	US-08-593-535-7
22	19	9.0	206	1	US-08-172-328-2
23	19	9.0	207	1	US-08-340-820-2
24	19	9.0	207	1	US-08-172-328-2
25	19	9.0	207	1	US-08-593-535-2
26	19	9.0	207	1	US-08-340-820-3
27	19	9.0	208	1	US-08-340-820-3

28	19	9.0	208	1	US-08-340-820-9	Sequence 9, Appli
29	19	9.0	208	1	US-08-340-820-25	Sequence 25, Appli
30	19	9.0	208	1	US-08-172-328-3	Sequence 3, Appli
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114 122 2.8 6 5304466-3 Patent No. 5304466
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135 175 2.8 6 US-08-902-233-8 Sequence 8, Appl
136 177 2.8 6 5430019-2 Patent No. 5430019
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139 187 2.8 6 PCT-US95-09172-11 Sequence 11, Appl
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146 198 2.8 6 US-08-718-904-15 Sequence 15, Appl
147 198 2.8 6 US-09-023-082A-14 Sequence 14, Appl
148 198 2.8 6 US-08-776-207-12 Sequence 12, Appl
149 198 2.8 6 PCT-US95-09172-12 Sequence 12, Appl
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152 205 2.8 6 5175383-6 Patent No. 5175383
153 206 2.8 6 US-08-102-691-1 Sequence 1, Appl
154 206 2.8 6 US-08-439-725A-13 Sequence 13, Appl
155 206 2.8 6 US-08-464-590A-15 Sequence 15, Appl
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171 206 2.8 6 PCT-US95-09172-10 Sequence 10, Appl
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173 207 2.8 6 US-08-902-233-5 Sequence 5, Appl

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178 208 2.8 6 US-08-951-822-27 Sequence 27, Appl
179 208 2.8 6 US-09-103-079-14 Sequence 14, Appl
180 208 2.8 6 US-08-902-233-6 Sequence 6, Appl
181 208 2.8 6 US-09-093-585-16 Sequence 16, Appl
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183 208 2.8 6 US-08-441-629-13 Sequence 13, Appl
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185 219 2.8 6 PCT-US95-09172-13 Sequence 13, Appl
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190 237 2.8 6 US-08-466-248-20 Sequence 20, Appl
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194 245 2.8 6 US-09-144-925-26 Sequence 26, Appl
195 266 2.8 6 US-08-815-809-5 Patent No. 5175383
196 266 2.8 6 5175383-5 Patent No. 5175383
197 267 2.8 6 US-08-462-169B-13 Sequence 13, Appl
198 267 2.8 6 US-09-103-079-13 Sequence 13, Appl
199 268 2.8 6 US-08-439-725A-12 Sequence 12, Appl
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242 358 2.8 6 US-08-462-300B-6 Sequence 6, Appl
243 358 2.8 6 US-08-463-074B-6 Sequence 6, Appl
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296	6	2.8	635	4	US-08-714-524D-36	Sequence 36, Appli	369	6	2.8	1861	2	US-08-790-912-4	Sequence 4, Appli
297	6	2.8	635	4	US-08-714-524D-50	Sequence 50, Appli	370	6	2.8	1911	1	US-08-348-006B-5	Sequence 5, Appli
298	6	2.8	650	4	US-09-232-191-29	Sequence 29, Appli	371	6	2.8	1911	2	US-08-800-825A-5	Sequence 5, Appli
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301	6	2.8	650	4	US-09-232-197-79	Sequence 79, Appli	374	6	2.8	2109	4	US-08-646-695-6	Sequence 6, Appli
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306	6	2.8	652	1	US-08-582-719-2	Sequence 2, Appli	379	6	2.8	2987	4	US-09-407-562-29	Sequence 29, Appli
307	6	2.8	655	4	US-09-232-191-31	Sequence 31, Appli	380	6	2.8	3170	2	US-07-642-734C-5	Sequence 5, Appli
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317	6	2.8	662	2	US-08-314-520-4	Sequence 4, Appli	390	6	2.8	15281	2	US-08-471-119A-2	Sequence 2, Appli
318	6	2.8	662	3	US-08-789-350-2	Sequence 2, Appli	391	6	2.4	5	1	US-07-969-307A-8	Sequence 8, Appli
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395	5	2.4	5	2	US-08-079-144-18	Sequence 18, Appl	468	18	3	US-08-928-694-38	Sequence 38, Appl
396	5	2.4	5	5	PCT-US94-026311-95	Sequence 95, Appl	469	18	5	PCT-US91-06950-35	Sequence 35, Appl
397	5	2.4	5	6	US-07-822-924-9	Sequence 9, Appl	470	18	5	PCT-US91-06950-38	Sequence 38, Appl
398	5	2.4	6	1	US-07-969-307A-11	Sequence 11, Appl	471	19	1	US-08-451-947-41	Sequence 41, Appl
399	5	2.4	6	2	US-09-060-455-18	Sequence 18, Appl	472	19	1	US-08-424-826A-41	Sequence 41, Appl
400	5	2.4	6	3	US-08-888-381-9	Sequence 9, Appl	473	19	2	US-08-793-490-5	Sequence 5, Appl
401	5	2.4	6	3	PCT-US93-00683-9	Sequence 9, Appl	474	19	3	US-08-928-694-41	Sequence 41, Appl
402	5	2.4	7	1	US-07-945-982-3	Sequence 3, Appl	475	19	5	PCT-US91-06950-41	Sequence 41, Appl
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404	5	2.4	7	1	US-08-372-455-3	Sequence 3, Appl	477	20	1	US-07-686-116A-4	Sequence 4, Appl
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407	5	2.4	8	6	5466668-42	Patent No. 5466668	480	20	1	US-07-895-252-7	Sequence 7, Appl
408	5	2.4	9	1	US-08-068-947-36	Sequence 36, Appl	481	20	1	US-08-072-283B-7	Sequence 7, Appl
409	5	2.4	9	1	US-08-215-805A-76	Sequence 76, Appl	482	20	1	US-08-637-759B-459	Sequence 459, App
410	5	2.4	9	4	US-09-258-754-57	Sequence 57, Appl	483	20	2	US-08-747-137-38	Sequence 38, Appl
411	5	2.4	9	4	US-09-042-107-57	Sequence 57, Appl	484	20	3	US-08-916-913A-6	Sequence 459, App
412	5	2.4	9	4	US-09-502-600-76	Sequence 76, Appl	485	20	3	US-08-871-355A-459	Sequence 6, Appl
413	5	2.4	9	4	US-09-502-600-91	Sequence 91, Appl	486	20	4	US-08-602-999A-109	Sequence 109, App
414	5	2.4	9	4	US-09-518-046-57	Sequence 57, Appl	487	20	4	US-09-247-527-18	Sequence 18, Appl
415	5	2.4	9	4	US-09-518-046-59	Sequence 59, Appl	488	20	4	US-09-439-313-492	Sequence 492, App
416	5	2.4	10	1	US-08-068-947-28	Sequence 28, Appl	489	20	4	US-09-439-313-570	Sequence 570, App
417	5	2.4	10	1	US-08-068-947-30	Sequence 30, Appl	490	20	4	US-09-201-945-459	Sequence 459, App
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421	5	2.4	10	3	US-09-139-762A-54	Sequence 54, Appl	494	23	1	US-08-251-472-5	Sequence 5, Appl
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423	5	2.4	10	4	US-09-025-596-33	Sequence 33, Appl	496	23	2	US-08-290-665A-252	Sequence 252, App
424	5	2.4	10	5	PCT-US95-04075-10	Sequence 10, Appl	497	23	3	US-08-105-904B-10	Sequence 10, Appl
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432	5	2.4	13	1	US-08-116-733-11	Sequence 11, Appl	505	24	1	US-08-484-635-125	Sequence 5, Appl
433	5	2.4	13	1	US-08-469-615-8	Sequence 8, Appl	506	24	1	US-08-484-635-125	Sequence 125, App
434	5	2.4	13	1	US-08-466-763-8	Sequence 8, Appl	507	24	2	US-08-484-631-125	Sequence 125, App
435	5	2.4	13	2	US-08-411-142A-8	Sequence 8, Appl	508	24	2	US-08-827-570-125	Sequence 13, Appl
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438	5	2.4	14	1	US-07-791-935B-9	Sequence 9, Appl	511	24	4	US-08-290-373B-6	Sequence 6, Appl
439	5	2.4	14	3	US-08-916-913A-11	Sequence 11, Appl	512	25	1	US-08-856-383-5	Sequence 5, Appl
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441	5	2.4	14	6	5164482-18	Patent No. 5164482	514	25	3	US-08-997-080-1	Sequence 1, Appl
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443	5	2.4	15	1	US-08-376-157B-5	Sequence 5, Appl	516	25	4	US-09-095-855-1	Sequence 1, Appl
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447	5	2.4	15	5	PCT-US94-05142-16	Sequence 16, Appl	520	26	3	US-07-776-272-16	Sequence 16, Appl
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454	5	2.4	17	2	US-08-290-853-18	Sequence 18, Appl	527	27	6	US-09-475-088-5	Sequence 5, Appl
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457	5	2.4	18	1	US-08-451-947-35	Sequence 35, Appl	530	29	2	US-08-488-351A-38	Sequence 1, Appl
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462	5	2.4	18	2	US-08-424-826A-38	Sequence 38, Appl	535	29	2	US-08-637-418-12	Sequence 12, Appl
463	5	2.4	18	2	US-08-471-282A-84	Sequence 84, Appl	536	29	2	US-08-637-418-13	Sequence 13, Appl
464	5	2.4	18	2	US-08-466-710C-84	Sequence 84, Appl	537	29	2	US-08-637-418-14	Sequence 14, Appl
465	5	2.4	18	3	US-08-468-739C-84	Sequence 84, Appl	538	29	2	US-08-846-762-49	Sequence 49, Appl

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542	5	2.4	30	1	US-07-596-081A-38	Sequence 38, Appl	615	5	2.4	49	1	US-08-365-981-7	Sequence 6, Appl
543	5	2.4	30	2	US-08-451-947-40	Sequence 40, Appl	616	5	2.4	49	4	US-09-027-900-6	Sequence 2, Appl
544	5	2.4	30	1	US-08-451-947-43	Sequence 43, Appl	617	5	2.4	50	4	US-09-031-902-2	Sequence 1, Appl
545	5	2.4	30	2	US-08-424-826A-40	Sequence 40, Appl	618	5	2.4	51	1	US-07-945-982-1	Sequence 1, Appl
546	5	2.4	30	3	US-08-424-826A-43	Sequence 43, Appl	619	5	2.4	51	1	US-08-372-455-1	Sequence 3, Appl
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548	5	2.4	30	3	US-08-928-694-43	Sequence 43, Appl	621	5	2.4	51	4	US-09-138-873A-3	Sequence 3, Appl
549	5	2.4	30	5	PCT-US91-06950-40	Sequence 40, Appl	622	5	2.4	52	1	US-08-247-475-38	Sequence 38, Appl
550	5	2.4	30	5	PCT-US91-06950-43	Sequence 43, Appl	623	5	2.4	52	1	US-08-479-650-38	Sequence 38, Appl
551	5	2.4	31	2	US-08-508-664-8	Sequence 8, Appl	624	5	2.4	52	1	US-08-191-866D-60	Sequence 60, Appl
552	5	2.4	31	4	US-08-905-223-410	Sequence 410, App	625	5	2.4	52	1	US-08-674-169-38	Sequence 38, Appl
553	5	2.4	31	6	5514646-6	Patent No. 5514646	626	5	2.4	52	2	US-08-185-949B-60	Sequence 60, Appl
554	5	2.4	32	1	US-07-596-081A-18	Sequence 18, Appl	627	5	2.4	52	4	US-09-227-357-537	Sequence 537, App
555	5	2.4	32	1	US-08-158-189-22	Sequence 22, Appl	628	5	2.4	53	1	US-08-014-153D-51	Sequence 51, Appl
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557	5	2.4	32	2	US-08-598-873-22	Sequence 22, Appl	630	5	2.4	53	1	US-08-014-153D-53	Sequence 53, Appl
558	5	2.4	32	3	US-08-938-548B-7	Sequence 7, Appl	631	5	2.4	53	1	US-08-014-153D-54	Sequence 54, Appl
559	5	2.4	32	3	US-08-484-322-63	Sequence 63, Appl	632	5	2.4	54	1	US-08-757-541-8	Sequence 8, Appl
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563	5	2.4	32	4	US-09-240-078-4	Sequence 4, Appl	636	5	2.4	54	2	US-08-660-963-17	Sequence 17, Appl
564	5	2.4	32	4	US-09-240-078-5	Sequence 5, Appl	637	5	2.4	54	2	US-08-660-963-18	Sequence 18, Appl
565	5	2.4	32	4	US-08-939-093A-7	Sequence 7, Appl	638	5	2.4	54	3	US-08-630-916A-118	Sequence 118, App
566	5	2.4	33	4	5514646-5	Patent No. 5514646	639	5	2.4	54	3	US-09-033-275-8	Sequence 8, Appl
567	5	2.4	33	4	US-09-091-814-66	Patent No. 5514646	640	5	2.4	54	4	US-09-342-581-8	Sequence 8, Appl
568	5	2.4	33	6	5514646-4	Patent No. 5514646	641	5	2.4	56	1	US-07-862-021B-16	Sequence 16, Appl
569	5	2.4	34	1	US-08-014-153D-2	Sequence 2, Appl	642	5	2.4	56	3	US-09-101-146-9	Sequence 9, Appl
570	5	2.4	34	1	US-08-014-153D-23	Sequence 23, Appl	643	5	2.4	56	5	PCT-US93-03164-16	Sequence 16, Appl
571	5	2.4	34	1	US-08-014-153D-30	Sequence 30, Appl	644	5	2.4	56	6	5514566-2	Patent No. 5514566
572	5	2.4	34	1	US-08-014-153D-31	Sequence 31, Appl	645	5	2.4	56	6	5514566-4	Patent No. 5514566
573	5	2.4	34	1	US-08-014-153D-32	Sequence 32, Appl	646	5	2.4	57	4	US-08-817-811-50	Sequence 50, Appl
574	5	2.4	34	1	US-08-014-153D-33	Sequence 33, Appl	647	5	2.4	57	4	US-09-039-211C-28	Sequence 28, Appl
575	5	2.4	34	1	US-08-014-153D-34	Sequence 34, Appl	648	5	2.4	58	1	US-07-743-518-22	Sequence 22, Appl
576	5	2.4	34	1	US-08-160-376A-3	Sequence 3, Appl	649	5	2.4	58	1	US-08-269-441A-11	Sequence 11, Appl
577	5	2.4	35	1	US-08-282-030-11	Sequence 11, Appl	650	5	2.4	58	1	US-08-451-947-42	Sequence 42, Appl
578	5	2.4	35	1	US-08-312-870-11	Sequence 11, Appl	651	5	2.4	58	1	US-08-464-531-84	Sequence 84, Appl
579	5	2.4	35	1	US-08-389-487-6	Sequence 6, Appl	652	5	2.4	58	2	US-08-424-826A-42	Sequence 42, Appl
580	5	2.4	35	2	US-09-134-836-3	Sequence 3, Appl	653	5	2.4	58	2	US-08-461-598-84	Sequence 84, Appl
581	5	2.4	35	2	PCT-US95-10219-11	Sequence 11, Appl	654	5	2.4	58	3	US-08-928-694-42	Sequence 42, Appl
582	5	2.4	35	6	5457066-1	Patent No. 5457066	655	5	2.4	58	3	US-08-322-137-84	Sequence 84, Appl
583	5	2.4	36	1	US-08-158-189-3	Sequence 3, Appl	656	5	2.4	58	4	US-09-518-046-6	Sequence 6, Appl
584	5	2.4	36	1	US-08-176-500-78	Sequence 78, Appl	657	5	2.4	58	5	PCT-US91-06950-42	Sequence 42, Appl
585	5	2.4	38	1	US-08-145-708A-16	Sequence 16, Appl	658	5	2.4	59	1	US-08-451-947-37	Sequence 37, Appl
586	5	2.4	38	1	US-08-471-052A-78	Sequence 78, Appl	659	5	2.4	59	1	US-08-485-455D-23	Sequence 23, Appl
587	5	2.4	38	1	US-08-189-331-78	Sequence 78, Appl	660	5	2.4	59	1	US-08-530-550-29	Sequence 29, Appl
588	5	2.4	38	2	US-08-471-939-78	Sequence 78, Appl	661	5	2.4	59	2	US-08-424-826A-37	Sequence 37, Appl
589	5	2.4	38	2	US-08-471-800-78	Sequence 78, Appl	662	5	2.4	59	2	US-08-482-130C-23	Sequence 23, Appl
590	5	2.4	38	2	US-08-471-068-78	Sequence 78, Appl	663	5	2.4	59	2	US-08-484-211C-23	Sequence 23, Appl
591	5	2.4	38	2	US-08-331-454-16	Sequence 16, Appl	664	5	2.4	59	3	US-08-928-694-37	Sequence 37, Appl
592	5	2.4	39	1	US-08-486-013-18	Sequence 18, Appl	665	5	2.4	59	3	US-08-906-769-23	Sequence 23, Appl
593	5	2.4	39	2	US-08-482-279-18	Sequence 18, Appl	666	5	2.4	59	3	US-08-906-616-23	Sequence 23, Appl
594	5	2.4	39	2	US-08-342-268-18	Sequence 18, Appl	667	5	2.4	59	4	US-08-817-795-23	Sequence 23, Appl
595	5	2.4	39	3	US-09-015-968-18	Sequence 18, Appl	668	5	2.4	59	4	US-08-485-443B-23	Sequence 23, Appl
596	5	2.4	39	4	US-09-397-386-18	Sequence 18, Appl	669	5	2.4	59	4	US-08-639-075A-23	Sequence 23, Appl
597	5	2.4	41	6	5514566-13	Patent No. 5514566	670	5	2.4	59	4	US-09-012-431-23	Sequence 23, Appl
598	5	2.4	43	1	US-07-745-206A-30	Sequence 30, Appl	671	5	2.4	59	4	US-09-012-692-23	Sequence 23, Appl
599	5	2.4	43	1	US-08-455-543A-57	Sequence 57, Appl	672	5	2.4	59	4	US-08-906-613-23	Sequence 23, Appl
600	5	2.4	43	2	US-08-223-305C-57	Sequence 57, Appl	673	5	2.4	59	5	PCT-US91-06950-37	Sequence 37, Appl
601	5	2.4	43	2	US-08-311-363-30	Sequence 30, Appl	674	5	2.4	59	5	PCT-US95-13660-29	Sequence 29, Appl
602	5	2.4	43	2	US-08-488-161-72	Sequence 72, Appl	675	5	2.4	59	5	PCT-US95-14442A-23	Sequence 23, Appl
603	5	2.4	43	2	US-08-488-161-80	Sequence 80, Appl	676	5	2.4	60	1	US-08-812-025-2	Sequence 2, Appl
604	5	2.4	43	2	US-08-499-676A-32	Sequence 32, Appl	677	5	2.4	60	4	US-09-138-873A-2	Sequence 2, Appl
605	5	2.4	43	3	US-09-273-685-72	Sequence 72, Appl	678	5	2.4	62	1	US-08-451-947-28	Sequence 28, Appl
606	5	2.4	43	3	US-09-273-685-80	Sequence 80, Appl	679	5	2.4	62	2	US-08-424-826A-28	Sequence 28, Appl
607	5	2.4	43	5	PCT-US95-11934-72	Sequence 72, Appl	680	5	2.4	62	3	US-08-928-694-28	Sequence 28, Appl
608	5	2.4	43	5	PCT-US95-11934-80	Sequence 80, Appl	681	5	2.4	62	3	PCT-US91-06950-28	Sequence 28, Appl
609	5	2.4	43	5	PCT-US95-11934-89	Sequence 89, Appl	682	5	2.4	63	1	US-08-616-732A-13	Sequence 13, Appl
610	5	2.4	43	5	US-09-100-600A-59	Sequence 59, Appl	683	5	2.4	63	4	US-09-037-742B-13	Sequence 13, Appl
611	5	2.4	46	1	US-08-446-692-40	Sequence 40, Appl	684	5	2.4	63	4	US-09-037-742B-13	Sequence 13, Appl

685	5	2.4	64	4	US-09-091-814-25	Sequence 25, Appl	758	5	2.4	81	3	US-09-249-448-7	Sequence 7, Appl
686	5	2.4	65	4	US-09-227-357-538	Sequence 538, App	759	5	2.4	81	4	US-08-817-811-55	Sequence 55, Appl
687	5	2.4	66	4	US-08-858-207A-535	Sequence 535, App	760	5	2.4	83	2	US-09-047-125-33	Sequence 33, Appl
688	5	2.4	67	2	US-08-588-258B-6	Sequence 6, Appl	761	5	2.4	83	3	US-07-736-335E-33	Sequence 33, Appl
689	5	2.4	67	3	US-08-460-505-6	Sequence 6, Appl	762	5	2.4	84	2	US-08-459-568-62	Sequence 62, Appl
690	5	2.4	67	5	PCT-US96-08295-6	Sequence 6, Appl	763	5	2.4	84	2	US-08-399-411-62	Sequence 62, Appl
691	5	2.4	68	1	US-08-315-695-1	Sequence 1, Appl	764	5	2.4	84	3	US-08-516-859A-62	Sequence 62, Appl
692	5	2.4	68	4	US-08-322-623-2	Sequence 2, Appl	765	5	2.4	85	3	US-08-222-617A-10	Sequence 10, Appl
693	5	2.4	68	4	US-09-188-930-123	Sequence 123, App	766	5	2.4	85	3	US-08-648-322-6	Sequence 6, Appl
694	5	2.4	71	3	US-08-616-732A-27	Sequence 27, Appl	767	5	2.4	86	1	US-07-715-183C-1	Sequence 1, Appl
695	5	2.4	71	3	US-08-513-974B-44	Sequence 44, Appl	768	5	2.4	86	4	US-09-382-155-8	Sequence 8, Appl
696	5	2.4	71	4	US-09-037-742B-27	Sequence 27, Appl	769	5	2.4	86	4	US-09-074-044A-8	Sequence 8, Appl
697	5	2.4	71	4	US-08-858-207A-458	Sequence 458, App	770	5	2.4	87	1	US-08-070-165F-2	Sequence 2, Appl
698	5	2.4	74	1	US-08-451-947-29	Sequence 29, Appl	771	5	2.4	87	2	US-08-865-418-2	Sequence 2, Appl
699	5	2.4	74	1	US-08-089-862-5	Sequence 5, Appl	772	5	2.4	88	1	US-08-308-086-11	Sequence 11, Appl
700	5	2.4	74	1	US-08-587-333-12	Sequence 12, Appl	773	5	2.4	88	2	US-08-690-011A-31	Sequence 31, Appl
701	5	2.4	74	2	US-08-424-826A-29	Sequence 29, Appl	774	5	2.4	88	3	US-08-513-974B-338	Sequence 338, App
702	5	2.4	74	3	US-08-928-694-29	Sequence 29, Appl	775	5	2.4	88	3	US-08-513-974B-339	Sequence 339, App
703	5	2.4	74	5	PCT-US91-06950-29	Sequence 29, Appl	776	5	2.4	89	1	US-08-167-035-22	Sequence 22, Appl
704	5	2.4	74	5	PCT-US94-07776-10	Sequence 10, Appl	777	5	2.4	89	1	US-08-208-887A-22	Sequence 22, Appl
705	5	2.4	75	4	US-08-817-811-97	Sequence 97, Appl	778	5	2.4	89	2	US-08-479-078-16	Sequence 16, Appl
706	5	2.4	76	2	US-08-244-537-6	Sequence 6, Appl	779	5	2.4	89	2	US-08-539-005-22	Sequence 22, Appl
707	5	2.4	76	4	US-08-817-811-21	Sequence 21, Appl	780	5	2.4	90	1	US-08-030-731A-43	Sequence 43, Appl
708	5	2.4	77	2	US-08-469-537A-44	Sequence 44, Appl	781	5	2.4	90	1	US-08-589-080-1	Sequence 1, Appl
709	5	2.4	77	2	US-08-465-380-4	Sequence 4, Appl	782	5	2.4	90	2	US-08-479-078-17	Sequence 17, Appl
710	5	2.4	77	2	US-08-465-380-40	Sequence 40, Appl	783	5	2.4	91	1	US-08-451-947-48	Sequence 48, Appl
711	5	2.4	77	2	US-08-480-478-33	Sequence 33, Appl	784	5	2.4	91	1	US-08-451-947-49	Sequence 49, Appl
712	5	2.4	77	2	US-08-486-397-4	Sequence 4, Appl	785	5	2.4	91	2	US-08-479-078-10	Sequence 10, Appl
713	5	2.4	77	2	US-08-486-397-40	Sequence 40, Appl	786	5	2.4	91	2	US-08-424-826A-48	Sequence 48, Appl
714	5	2.4	77	2	US-08-486-399-4	Sequence 4, Appl	787	5	2.4	91	2	US-08-424-826A-49	Sequence 49, Appl
715	5	2.4	77	2	US-08-486-399-40	Sequence 40, Appl	788	5	2.4	91	2	US-08-637-759B-60	Sequence 60, Appl
716	5	2.4	77	2	US-08-461-965-4	Sequence 4, Appl	789	5	2.4	91	2	US-09-047-125-31	Sequence 31, Appl
717	5	2.4	77	2	US-08-461-965-40	Sequence 40, Appl	790	5	2.4	91	3	US-08-871-355A-60	Sequence 60, Appl
718	5	2.4	77	2	US-08-326-110A-33	Sequence 33, Appl	791	5	2.4	91	3	US-08-928-694-48	Sequence 48, Appl
719	5	2.4	77	2	US-08-634-641-4	Sequence 4, Appl	792	5	2.4	91	3	US-08-928-694-49	Sequence 49, Appl
720	5	2.4	77	2	US-08-634-641-40	Sequence 40, Appl	793	5	2.4	91	3	US-07-736-335E-31	Sequence 31, Appl
721	5	2.4	77	2	US-08-726-306A-174	Sequence 174, App	794	5	2.4	91	4	US-09-201-945-60	Sequence 60, Appl
722	5	2.4	77	3	US-09-249-471-4	Sequence 4, Appl	795	5	2.4	91	5	PCT-US91-06950-48	Sequence 48, Appl
723	5	2.4	77	3	US-09-249-471-40	Sequence 40, Appl	796	5	2.4	91	5	PCT-US91-06950-49	Sequence 49, Appl
724	5	2.4	77	3	US-08-819-177-17	Sequence 17, Appl	797	5	2.4	92	1	US-08-451-947-50	Sequence 50, Appl
725	5	2.4	77	3	US-09-249-472-4	Sequence 4, Appl	798	5	2.4	92	2	US-08-424-826A-50	Sequence 50, Appl
726	5	2.4	77	3	US-09-249-472-40	Sequence 40, Appl	799	5	2.4	92	3	US-08-928-694-50	Sequence 50, Appl
727	5	2.4	77	3	US-09-249-451-4	Sequence 4, Appl	800	5	2.4	92	5	PCT-US91-06950-50	Sequence 50, Appl
728	5	2.4	77	3	US-09-249-451-40	Sequence 40, Appl	801	5	2.4	93	2	US-08-821-009-3	Sequence 3, Appl
729	5	2.4	77	3	US-08-809-455-4	Sequence 4, Appl	802	5	2.4	93	2	US-09-099-572-3	Sequence 3, Appl
730	5	2.4	77	3	US-08-809-455-40	Sequence 40, Appl	803	5	2.4	93	4	US-09-142-078-64	Sequence 64, Appl
731	5	2.4	77	3	US-09-249-461-4	Sequence 4, Appl	804	5	2.4	93	4	US-09-357-141-64	Sequence 64, Appl
732	5	2.4	77	3	US-09-249-461-40	Sequence 40, Appl	805	5	2.4	94	1	US-08-158-189-5	Sequence 5, Appl
733	5	2.4	77	3	US-09-249-448-4	Sequence 4, Appl	806	5	2.4	95	2	US-08-530-569B-3	Sequence 3, Appl
734	5	2.4	77	3	US-09-249-448-40	Sequence 40, Appl	807	5	2.4	95	4	US-09-142-078-66	Sequence 66, Appl
735	5	2.4	78	2	US-08-475-035-1	Sequence 1, Appl	808	5	2.4	96	2	US-09-357-141-66	Sequence 66, Appl
736	5	2.4	79	2	US-09-174-060-1	Sequence 1, Appl	809	5	2.4	96	2	US-09-134-836-4	Sequence 4, Appl
737	5	2.4	79	2	US-08-499-676A-13	Sequence 13, Appl	810	5	2.4	96	2	US-09-134-836-5	Sequence 5, Appl
738	5	2.4	79	3	US-08-819-177-16	Sequence 16, Appl	811	5	2.4	96	4	US-08-818-112-102	Sequence 102, App
739	5	2.4	79	3	US-08-338-382-1	Sequence 1, Appl	812	5	2.4	96	4	US-08-818-111-97	Sequence 97, Appl
740	5	2.4	80	3	US-09-081-320-9	Sequence 9, Appl	813	5	2.4	96	4	US-09-056-556-102	Sequence 102, App
741	5	2.4	80	3	US-09-081-320-20	Sequence 20, Appl	814	5	2.4	97	1	US-08-160-376A-4	Sequence 4, Appl
742	5	2.4	80	3	US-09-081-320-31	Sequence 31, Appl	815	5	2.4	97	1	US-08-389-487-7	Sequence 7, Appl
743	5	2.4	80	4	US-08-714-071-2	Sequence 2, Appl	816	5	2.4	97	1	US-08-150-203A-3	Sequence 3, Appl
744	5	2.4	80	4	US-08-936-165A-425	Sequence 425, App	817	5	2.4	97	1	US-08-454-730-3	Sequence 3, Appl
745	5	2.4	81	2	US-08-602-093-3	Sequence 3, Appl	818	5	2.4	97	4	US-09-099-307-6	Sequence 6, Appl
746	5	2.4	81	2	US-08-465-380-7	Sequence 7, Appl	819	5	2.4	97	4	US-09-099-307-7	Sequence 7, Appl
747	5	2.4	81	2	US-08-480-478-36	Sequence 36, Appl	820	5	2.4	97	4	US-09-099-307-8	Sequence 8, Appl
748	5	2.4	81	2	US-08-486-397-7	Sequence 7, Appl	821	5	2.4	97	4	US-09-099-307-11	Sequence 11, Appl
749	5	2.4	81	2	US-08-486-399-7	Sequence 7, Appl	822	5	2.4	98	2	US-08-242-097-4	Sequence 4, Appl
750	5	2.4	81	2	US-08-461-965-7	Sequence 7, Appl	823	5	2.4	98	3	US-08-946-329A-87	Sequence 87, Appl
751	5	2.4	81	2	US-08-326-110A-36	Sequence 36, Appl	824	5	2.4	98	4	US-09-206-695-4	Sequence 4, Appl
752	5	2.4	81	2	US-08-634-641-7	Sequence 7, Appl	825	5	2.4	98	4	US-08-123-934A-12	Sequence 12, Appl
753	5	2.4	81	3	US-09-249-471-7	Sequence 7, Appl	826	5	2.4	98	5	PCT-US94-10080-12	Sequence 12, Appl
754	5	2.4	81	3	US-09-249-472-7	Sequence 7, Appl	827	5	2.4	99	1	US-08-333-358-4	Sequence 4, Appl
755	5	2.4	81	3	US-09-249-451-7	Sequence 7, Appl	828	5	2.4	99	1	US-08-463-694-4	Sequence 4, Appl
756	5	2.4	81	3	US-08-809-455-7	Sequence 7, Appl	829	5	2.4	99	1	US-08-694-501-4	Sequence 4, Appl
757	5	2.4	81	3	US-09-249-461-7	Sequence 7, Appl	830	5	2.4	100	2	US-08-465-380-20	Sequence 20, Appl

831	5	2.4	100	2	US-08-480-478-48	Sequence 48, Appl	904	4	US-08-785-371-4	Sequence 4, Appl
832	5	2.4	100	2	US-08-486-397-20	Sequence 20, Appl	905	5	PCT-US95-08596-2	Sequence 2, Appl
833	5	2.4	100	2	US-08-486-399-20	Sequence 20, Appl	906	5	US-09-097-767A-35	Sequence 35, Appl
834	5	2.4	100	2	US-08-461-965-20	Sequence 20, Appl	907	5	US-08-905-223-468	Sequence 468, Appl
835	5	2.4	100	2	US-08-326-110A-48	Sequence 48, Appl	908	5	US-08-648-322-2	Sequence 2, Appl
836	5	2.4	100	2	US-08-634-641-20	Sequence 20, Appl	909	5	US-08-899-330-3	Sequence 3, Appl
837	5	2.4	100	2	US-08-726-306A-129	Sequence 129, Appl	910	5	US-08-899-330-4	Sequence 4, Appl
838	5	2.4	100	2	US-09-249-471-20	Sequence 20, Appl	911	5	US-09-001-472-3	Sequence 3, Appl
839	5	2.4	100	3	US-09-034-916-13	Sequence 13, Appl	912	5	US-08-326-117B-8	Sequence 8, Appl
840	5	2.4	100	3	US-09-249-472-20	Sequence 20, Appl	913	5	US-08-710-330A-1	Sequence 1, Appl
841	5	2.4	100	3	US-09-249-451-20	Sequence 20, Appl	914	5	US-08-710-330A-2	Sequence 2, Appl
842	5	2.4	100	3	US-08-809-455-20	Sequence 20, Appl	915	5	US-08-710-330A-3	Sequence 3, Appl
843	5	2.4	100	3	US-09-249-461-20	Sequence 20, Appl	916	5	US-08-710-330A-4	Sequence 4, Appl
844	5	2.4	100	3	US-09-249-448-20	Sequence 20, Appl	917	5	US-08-710-330A-5	Sequence 5, Appl
845	5	2.4	100	4	US-09-142-078-46	Sequence 46, Appl	918	5	US-08-466-860-9	Sequence 9, Appl
846	5	2.4	100	4	US-09-247-527-2	Sequence 2, Appl	919	5	US-08-466-860-10	Sequence 10, Appl
847	5	2.4	100	4	US-09-357-141-46	Sequence 46, Appl	920	5	US-08-982-129-8	Sequence 8, Appl
848	5	2.4	101	2	US-08-466-860-75	Sequence 75, Appl	921	5	US-08-472-040A-9	Sequence 9, Appl
849	5	2.4	101	3	US-08-472-040A-75	Sequence 75, Appl	922	5	US-08-472-040A-10	Sequence 10, Appl
850	5	2.4	101	4	US-08-276-776-75	Sequence 75, Appl	923	5	US-08-276-776-9	Sequence 9, Appl
851	5	2.4	101	4	US-08-471-203-75	Sequence 75, Appl	924	5	US-08-276-776-10	Sequence 10, Appl
852	5	2.4	101	4	US-09-199-637A-3	Sequence 3, Appl	925	5	US-08-471-209-9	Sequence 9, Appl
853	5	2.4	102	2	US-08-840-683-12	Sequence 12, Appl	926	5	US-08-471-209-10	Sequence 10, Appl
854	5	2.4	102	2	US-09-174-060-2	Sequence 2, Appl	927	5	US-08-451-947-58	Sequence 58, Appl
855	5	2.4	102	2	US-08-555-722-12	Sequence 12, Appl	928	5	US-08-424-826A-58	Sequence 58, Appl
856	5	2.4	102	3	US-09-122-443-5	Sequence 5, Appl	929	5	PCT-US91-06950-58	Sequence 58, Appl
857	5	2.4	102	3	US-08-338-382-2	Sequence 2, Appl	930	5	US-08-853-659A-58	Sequence 58, Appl
858	5	2.4	102	3	US-08-894-173-75	Sequence 75, Appl	931	5	US-08-846-134-1	Sequence 1, Appl
859	5	2.4	102	3	US-08-654-618-25	Sequence 25, Appl	932	5	US-09-056-556-198	Sequence 198, Appl
860	5	2.4	102	3	US-08-654-575-25	Sequence 25, Appl	933	5	US-08-650-262-4	Sequence 4, Appl
861	5	2.4	102	4	US-08-444-818-144	Sequence 144, Appl	934	5	US-08-818-112-85	Sequence 85, Appl
862	5	2.4	102	4	US-09-398-193-75	Sequence 75, Appl	935	5	US-08-818-111-86	Sequence 86, Appl
863	5	2.4	102	4	US-09-384-301-12	Sequence 12, Appl	936	5	US-09-056-556-85	Sequence 85, Appl
864	5	2.4	103	1	US-08-451-947-30	Sequence 30, Appl	937	5	US-09-199-637A-87	Sequence 87, Appl
865	5	2.4	103	2	US-08-424-826A-30	Sequence 30, Appl	938	5	US-09-188-930-168	Sequence 168, Appl
866	5	2.4	103	3	US-08-928-694-30	Sequence 30, Appl	939	5	US-08-946-329A-104	Sequence 104, Appl
867	5	2.4	103	3	US-09-027-381-4	Sequence 4, Appl	940	5	US-08-890-865A-14	Sequence 14, Appl
868	5	2.4	103	4	US-09-370-253-14	Sequence 14, Appl	941	5	US-08-936-165A-357	Sequence 357, Appl
869	5	2.4	103	4	US-09-477-071-4	Sequence 4, Appl	942	5	US-08-249-013-5	Sequence 5, Appl
870	5	2.4	104	1	PCT-US91-06950-30	Sequence 30, Appl	943	5	US-08-886-863-5	Sequence 5, Appl
871	5	2.4	104	1	US-08-700-626-3	Sequence 3, Appl	944	5	US-09-175-229-5	Sequence 5, Appl
872	5	2.4	104	1	US-08-340-203A-9	Sequence 9, Appl	945	5	PCT-US95-06764-5	Sequence 5, Appl
873	5	2.4	104	2	US-08-452-427-9	Sequence 9, Appl	946	5	US-07-893-929A-4	Sequence 4, Appl
874	5	2.4	104	3	US-09-085-407-9	Sequence 9, Appl	947	5	US-08-061-314A-2	Sequence 2, Appl
875	5	2.4	104	3	US-08-654-618-21	Sequence 21, Appl	948	5	US-08-938-548B-10	Sequence 10, Appl
876	5	2.4	104	3	US-08-654-575-7	Sequence 7, Appl	949	5	US-09-188-930-292	Sequence 292, Appl
877	5	2.4	105	1	US-08-451-947-31	Sequence 31, Appl	950	5	PCT-US92-10344-4	Sequence 4, Appl
878	5	2.4	105	1	US-08-417-460-6	Sequence 6, Appl	951	5	US-08-451-947-55	Sequence 55, Appl
879	5	2.4	105	2	US-08-424-826A-31	Sequence 31, Appl	952	5	US-08-424-826A-55	Sequence 55, Appl
880	5	2.4	105	3	US-08-928-694-31	Sequence 31, Appl	953	5	US-08-981-189B-15	Sequence 15, Appl
881	5	2.4	105	4	US-08-881-189B-13	Sequence 13, Appl	954	5	PCT-US91-06950-55	Sequence 55, Appl
882	5	2.4	105	5	PCT-US91-06950-31	Sequence 31, Appl	955	5	US-08-451-947-57	Sequence 57, Appl
883	5	2.4	106	1	US-07-634-278-8	Sequence 8, Appl	956	5	US-08-424-826A-57	Sequence 57, Appl
884	5	2.4	106	1	US-08-477-728-8	Sequence 8, Appl	957	5	US-08-244-205-15	Sequence 15, Appl
885	5	2.4	106	1	US-08-474-040-8	Sequence 8, Appl	958	5	PCT-US91-06950-57	Sequence 57, Appl
886	5	2.4	106	1	US-08-487-200-8	Sequence 8, Appl	959	5	PCT-US92-10284-15	Sequence 15, Appl
887	5	2.4	106	1	US-08-967-513-4	Sequence 4, Appl	960	5	US-09-329-884-8	Sequence 8, Appl
888	5	2.4	106	2	US-08-687-645B-4	Sequence 4, Appl	961	5	US-08-858-207A-479	Sequence 479, Appl
889	5	2.4	106	3	US-08-946-329A-76	Sequence 76, Appl	962	5	US-08-804-439A-4	Sequence 4, Appl
890	5	2.4	106	4	US-08-484-537-8	Sequence 8, Appl	963	5	US-08-720-229-4	Sequence 4, Appl
891	5	2.4	107	2	US-08-553-541B-4	Sequence 4, Appl	964	5	US-08-451-947-53	Sequence 53, Appl
892	5	2.4	107	2	US-08-810-572A-4	Sequence 4, Appl	965	5	US-08-451-947-54	Sequence 54, Appl
893	5	2.4	107	4	US-09-268-202-4	Sequence 4, Appl	966	5	US-08-424-826A-53	Sequence 53, Appl
894	5	2.4	107	4	US-09-290-333-4	Sequence 4, Appl	967	5	US-08-424-826A-54	Sequence 54, Appl
895	5	2.4	107	3	US-08-894-173-95	Sequence 95, Appl	968	5	US-08-928-694-53	Sequence 53, Appl
896	5	2.4	109	4	US-09-398-193-95	Sequence 95, Appl	969	5	PCT-US91-06950-53	Sequence 53, Appl
897	5	2.4	110	2	US-08-244-537-10	Sequence 10, Appl	970	5	US-08-451-947-55	Sequence 55, Appl
898	5	2.4	110	3	US-08-950-720A-11	Sequence 11, Appl	971	5	US-08-424-826A-54	Sequence 54, Appl
899	5	2.4	110	3	US-08-589-028-2	Sequence 2, Appl	972	5	US-08-928-694-53	Sequence 53, Appl
900	5	2.4	110	3	US-08-589-028-4	Sequence 4, Appl	973	5	US-08-928-694-53	Sequence 53, Appl
901	5	2.4	110	3	US-08-784-582-2	Sequence 2, Appl	974	5	US-09-199-637A-371	Sequence 371, Appl
902	5	2.4	110	3	US-08-784-582-4	Sequence 4, Appl	975	5	PCT-US91-06950-53	Sequence 53, Appl
903	5	2.4	110	4	US-08-785-271-2	Sequence 2, Appl	976	5		

977 5 2.4 129 5 PCT-US91-06950-54 Sequence 54, Appl
978 5 2.4 130 1 US-08-451-947-13 Sequence 13, Appl
979 5 2.4 130 1 US-08-451-947-14 Sequence 14, Appl
980 5 2.4 130 1 US-08-451-947-15 Sequence 15, Appl
981 5 2.4 130 1 US-08-451-947-16 Sequence 16, Appl
982 5 2.4 130 1 US-08-451-947-17 Sequence 17, Appl
983 5 2.4 130 1 US-08-451-947-18 Sequence 18, Appl
984 5 2.4 130 1 US-08-451-947-19 Sequence 19, Appl
985 5 2.4 130 1 US-08-451-947-20 Sequence 20, Appl
986 5 2.4 130 1 US-08-451-947-21 Sequence 21, Appl
987 5 2.4 130 1 US-08-451-947-22 Sequence 22, Appl
988 5 2.4 130 1 US-08-451-947-23 Sequence 23, Appl
989 5 2.4 130 1 US-08-451-947-47 Sequence 47, Appl
990 5 2.4 130 1 US-08-451-947-59 Sequence 59, Appl
991 5 2.4 130 1 US-08-451-947-60 Sequence 60, Appl
992 5 2.4 130 1 US-08-451-947-61 Sequence 61, Appl
993 5 2.4 130 1 US-08-451-947-62 Sequence 62, Appl
994 5 2.4 130 1 US-08-451-947-63 Sequence 63, Appl
995 5 2.4 130 1 US-08-451-947-64 Sequence 64, Appl
996 5 2.4 130 1 US-08-451-947-65 Sequence 65, Appl
997 5 2.4 130 1 US-08-451-947-66 Sequence 66, Appl
998 5 2.4 130 1 US-08-451-947-67 Sequence 67, Appl
999 5 2.4 130 1 US-08-451-947-68 Sequence 68, Appl
1000 5 2.4 130 1 US-08-451-947-69 Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-08-340-820-1
; Sequence 1, Application US/08340820
; Patent No. 5512460
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/340,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/07/835,713
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-08-340-820-1
Query Match 9.0%; Score 19; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 AVGLVSIRGVDSGLYGMN 122
Db 48 AVGLVSIRGVDSGLYGMN 66
|||||
RESULT 2
US-08-172-328-1
; Sequence 1, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/POCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cdna library
; CLONE: pGAF1
US-08-172-328-1
Query Match 9.0%; Score 19; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 104 AVGLVSIRGVDSGLYGMN 122
Db 48 AVGLVSIRGVDSGLYGMN 66
|||||

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RESULT 3
US-08-593-535-1
; Sequence 1, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; TITLE OF INVENTION: PRODUCTION
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
; US-08-172-328-8
;
; Query Match 9.0%; Score 19; DB 1; Length 159;
; Best Local Similarity 100.0%; Pred. No. 6e-11;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 104 AVGLVSRGVDSGLYLGMN 122
| | | | | | | | | | | | | | | | | | | | | |
Db 52 AVGLVSRGVDSGLYLGMN 70

RESULT 5
US-08-172-328-9
; Sequence 9, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; Query Match 9.0%; Score 19; DB 1; Length 142;
; Best Local Similarity 100.0%; Pred. No. 5.5e-11;
; Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 104 AVGLVSRGVDSGLYLGMN 122
| | | | | | | | | | | | | | | | | | | | | |
Db 48 AVGLVSRGVDSGLYLGMN 66

RESULT 4
US-08-172-328-8
; Sequence 8, Application US/08172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; TITLE OF INVENTION: USE THEREOF
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
```

```

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
; US-08-172-328-9

Query Match          9.0%; Score 19; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 6.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AVGLVSIRGVDGSLYLGNN 122
Db 53 AVGLVSIRGVDGSLYLGNN 71

RESULT 6
US-08-172-328-6
; Sequence 6, Application US/08/172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 160 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
; US-08-172-328-9

;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
; US-08-172-328-6

Query Match          9.0%; Score 19; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 6.6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 104 AVGLVSIRGVDGSLYLGNN 122
Db 68 AVGLVSIRGVDGSLYLGNN 86

RESULT 7
US-08-172-328-7
; Sequence 7, Application US/08/172328
; Patent No. 5571895
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KUROSHIMA, Ken-ichi
; APPLICANT: YOSHITOMI, Sumie
; APPLICANT: SEKO, Sachiko
; TITLE OF INVENTION: ANTIBODIES, POLYPEPTIDES, PRODUCTION AND
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/172,328
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964
; REFERENCE/DOCKET NUMBER: 26964
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 176 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; HAPLOTYPE: 2n
; TISSUE TYPE: Skin
; CELL TYPE: Fibroblast
; IMMEDIATE SOURCE:
; LIBRARY: Human foreskin cDNA library
; CLONE: pGAF1
; US-08-172-328-6
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ORGANISM: Homo sapiens
HAPLOTYPE: 2n
TISSUE TYPE: Skin
CELL TYPE: Fibroblast
IMMEDIATE SOURCE:
LIBRARY: Human foreskin cDNA library
CLONE: pGAF1
US-08-172-328-7

Query Match 9.0%; Score 19; DB 1; Length 176;
Best Local Similarity 100.0%; Pred. No. 6.6e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIKGVDSGLYLGMN 122
|||||
Db 69 AVGLVSIKGVDSGLYLGMN 87

RESULT 8
US-08-340-820-4
; Sequence 4, Application US/08340820
; Patent No. 5512460
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340.820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/835,713
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-340-820-4

Query Match 9.0%; Score 19; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIKGVDSGLYLGMN 122
|||||
Db 70 AVGLVSIKGVDSGLYLGMN 88

RESULT 9
US-08-593-535-4
; Sequence 4, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-593-535-4

Query Match 9.0%; Score 19; DB 1; Length 177;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIKGVDSGLYLGMN 122
|||||
Db 70 AVGLVSIKGVDSGLYLGMN 88

RESULT 10
US-08-340-820-6
; Sequence 6, Application US/08340820
; Patent No. 5512460
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street

```

; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,820
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/835,713
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-340-820-6

Query Match          9.0%; Score 19; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDGSLYLGNN 122
DB 71 AVGLVSIRGVDGSLYLGNN 89

RESULT 11
US-08-593-535-6
; Sequence 6, Application US/08593535
; Patent No. 5622928
; GENERAL INFORMATION:
; APPLICANT: NARUO, Ken-ichi
; APPLICANT: SEKO, Chisako
; APPLICANT: KUROKAWA, Tsutomu
; APPLICANT: KONDO, Tatsuya
; TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/593,535
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/835,713
; FILING DATE: 12-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G.
; REGISTRATION NUMBER: 27026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 178 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-340-820-6

Query Match          9.0%; Score 19; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 6.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDGSLYLGNN 122
DB 71 AVGLVSIRGVDGSLYLGNN 89

RESULT 12
US-08-441-629-16
; Sequence 16, Application US/08441629
; Patent No. 5766923
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, No. 5766923iyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millicia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,629
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/279,217
; FILING DATE: 22-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: H095-01A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-441-629-16

Query Match          9.0%; Score 19; DB 1; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDGSLYLGNN 122
DB 71 AVGLVSIRGVDGSLYLGNN 89
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Db 101 AVGLVSIRGVDSGLYLGMN 119

RESULT 13

US-08-776-207-16
; Sequence 16, Application US/08776207A
; Patent No. 6080718
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Receptor-Ligand Assay
; FILE REFERENCE: HU95-01A2
; CURRENT APPLICATION NUMBER: US/08/776,207A
; CURRENT FILING DATE: 1997-06-23
; EARLIER APPLICATION NUMBER: PCT/US95/09172
; EARLIER FILING DATE: 1995-07-19
; EARLIER APPLICATION NUMBER: 08/441,629
; EARLIER FILING DATE: 1995-05-15
; EARLIER APPLICATION NUMBER: 08/279,217
; EARLIER FILING DATE: 1994-07-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapien
US-08-776-207-16

Query Match 9.0%; Score 19; DB 3; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
Db 101 AVGLVSIRGVDSGLYLGMN 119

RESULT 14

PCT-US95-09172-16
; Sequence 16, Application PC/TUS9509172
; GENERAL INFORMATION:
; APPLICANT: Kirschner, Marc W.
; APPLICANT: Kinoshita, Noriyuki
; TITLE OF INVENTION: RECEPTOR-LIGAND ASSAY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/09172
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/279,217
; FILING DATE: 22-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/441,629
; FILING DATE: 15-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: HU95-01A PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240

; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 190 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-09172-16

Query Match 9.0%; Score 19; DB 5; Length 190;
Best Local Similarity 100.0%; Pred. No. 7.1e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
Db 101 AVGLVSIRGVDSGLYLGMN 119

RESULT 15

US-08-438-439C-21
; Sequence 21, Application US/08438439C
; Patent No. 5876967
; GENERAL INFORMATION:
; APPLICANT: Nathans, Jeremy
; APPLICANT: Smallwood, Phillip M.
; APPLICANT: Macke, Jennifer P.
; TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR HOMOLOGOUS
; TITLE OF INVENTION: FACTOR-2 AND METHODS OF USE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,439C
; FILING DATE: May 12, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/046001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-438-439C-21

Query Match 9.0%; Score 19; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 7.2e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
Db 101 AVGLVSIRGVDSGLYLGMN 119

Search completed: October 21, 2002, 16:21:17
Job time : 32 secs

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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:17:56 ; Search time 20 Seconds
(without alignments)
1013.742 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 211

Sequence: 1 MAPLAEGGFLGLEGLGQQ.....PRPVDPERVELYKDLLMYT 211

Scoring table:

OLIGO

Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	85	40.3	212	2	JC7511
3	26	12.3	208	2	JC7082
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5	19	9.0	208	2	A48137
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7	16	7.6	207	2	JC5941
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9	8	3.8	157	2	G87417
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11	8	3.8	226	2	T01363
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13	8	3.8	564	2	F59092
14	8	3.8	756	2	T00367
15	8	3.8	1020	2	T42229
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18	7	3.3	101	2	D82716
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21	7	3.3	156	2	S41784
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23	7	3.3	167	2	B98088
24	7	3.3	177	2	F82324
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31	7	3.3	246	1	A32999
32	7	3.3	251	2	F87242
33	7	3.3	255	2	S21498
34	7	3.3	262	2	T22599
35	7	3.3	262	2	T01305
36	7	3.3	267	2	H72590
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38	7	3.3	278	2	E83336
39	7	3.3	314	2	S75685
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46	7	3.3	392	1	A70406
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49	7	3.3	413	2	H88481
50	7	3.3	415	2	S37340
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57	7	3.3	439	2	D72716
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59	7	3.3	492	2	A35354
60	7	3.3	496	2	D97023
61	7	3.3	511	1	A48560
62	7	3.3	512	1	WMBEY4
63	7	3.3	589	2	T12820
64	7	3.3	627	1	JC6534
65	7	3.3	657	2	H71422
66	7	3.3	709	2	JH0126
67	7	3.3	709	2	AE3468
68	7	3.3	711	1	TFHUL
69	7	3.3	738	2	E85061
70	7	3.3	739	2	S06397
71	7	3.3	757	2	T42693
72	7	3.3	824	2	AD3098
73	7	3.3	829	2	F83499
74	7	3.3	829	2	D82430
75	7	3.3	834	2	B95346
76	7	3.3	834	2	E98188
77	7	3.3	863	2	T38016
78	7	3.3	875	2	F96027
79	7	3.3	1012	2	T13603
80	7	3.3	1025	2	S69790
81	7	3.3	1058	2	B95292
82	7	3.3	1128	1	Q0BE47
83	7	3.3	1418	2	D75281
84	7	3.3	1536	2	S59841
85	7	3.3	1607	2	T02837
86	7	3.3	2163	2	T15276
87	7	3.3	3390	1	GNWVD3
88	7	3.3	4302	2	A38971
89	7	3.3	13055	2	T16580
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92	6	2.8	47	2	S78335
93	6	2.8	56	1	CBBOC6
94	6	2.8	57	2	S07344
95	6	2.8	61	2	G95882
96	6	2.8	64	2	B82672
97	6	2.8	66	2	S61083
98	6	2.8	68	2	I40461
99	6	2.8	78	2	S69531
100	6	2.8	86	2	JH0445
101	6	2.8	86	2	A96968
102	6	2.8	90	2	C84841

glutathione peroxi
myelin P0 protein
probable secreted
bclA protein - Rho
1-acylglycerol-3-p
hypothetical prote
hypothetical prote
hypothetical prote
cytochrome c bioge
hypothetical prote
hypothetical prote
hypothetical prote
multidrug resistan
polymerase-associa
transporter (major
transcription acti
LFY floral meriste
protein let-756 (i
LFY floral meriste
probable glutamate
LFY floral meriste
tolB protein, prob
probable polysacch
regulatory protein
hypothetical prote
hypothetical prote
UL 41 protein - hu
threonine synthase
UL54 protein - hum
hypothetical prote
protein kinase 1 (
hypothetical prote
moA protein precu
diacylate cyclas
lactotransferrin p
probable homeotic
photosystem I prot
hypothetical prote
periplasmic nitrat
periplasmic nitrat
NAPa periplasmic n
periplasmic nitrat
importin beta-1 su
probable maltoolig
probable N-methyl-
fibronectin-bindin
probable adenylate
DNA-binding protei
ribonucleoside-dip
4-alpha-glucanotra
long chain fatty a
hypothetical prote
genome polyprotein
polycystic kidney
hypothetical prote
probable phospholi
hypothetical prote
hypothetical prote
cytochrome b-c1 co
nef protein - huma
hypothetical prote
hypothetical prote
M protein precurs
mersacidin precurs
holin protein - ph
hypothetical 10.2K
hypothetical prote
hypothetical prote

103	6	2.8	91	2	G75015	acetylphosphatase (a	176	6	2.8	178	2	S00528	vegA protein - Myx
104	6	2.8	95	2	T17894	hypothetical prote	177	6	2.8	180	2	D83636	conserved hypothet
105	6	2.8	99	2	B84841	hypothetical prote	178	6	2.8	182	2	S03247	nef protein (clone
106	6	2.8	100	2	D72708	hypothetical prote	179	6	2.8	183	2	E82212	hypothetical prote
107	6	2.8	101	2	AG3458	urease beta chain	180	6	2.8	184	2	C83373	hypothetical prote
108	6	2.8	101	2	C90239	acetylphosphatase [i	181	6	2.8	184	2	H75329	conserved hypothet
109	6	2.8	106	2	D97815	hypothetical prote	182	6	2.8	185	2	T36874	hypothetical prote
110	6	2.8	107	1	B36950	urease (EC 3.5.1.5	183	6	2.8	187	2	S23595	embryonic fibrobla
111	6	2.8	107	2	H84658	hypothetical prote	184	6	2.8	188	1	F64494	conserved hypothet
112	6	2.8	108	2	AE2264	urease beta chain	185	6	2.8	188	1	H70042	transcription regu
113	6	2.8	112	2	S40292	protein-tyrosine-p	186	6	2.8	191	2	B84272	protoporphyrinogen
114	6	2.8	111	2	G34768	hypothetical prote	187	6	2.8	191	2	AG3068	conserved hypothet
115	6	2.8	112	2	A13297	hypothetical prote	188	6	2.8	191	2	D98218	hypothetical prote
116	6	2.8	114	2	T33802	hypothetical prote	189	6	2.8	191	2	G90966	hypothetical prote
117	6	2.8	115	2	S22738	hypothetical prote	190	6	2.8	191	2	G85814	probable outer mem
118	6	2.8	117	2	A89964	hypothetical prote	191	6	2.8	192	2	S54407	embryonic fibrobla
119	6	2.8	118	1	B70021	arsenate reductase	192	6	2.8	193	2	H91249	hypothetical prote
120	6	2.8	118	2	T03756	hypothetical prote	193	6	2.8	194	2	I50710	fibroblast growth
121	6	2.8	121	1	S10031	hypothetical prote	194	6	2.8	197	2	S25106	capsid protein - b
122	6	2.8	121	2	H72507	urease (EC 3.5.1.5	195	6	2.8	198	2	S48749	cytochrome P460 pr
123	6	2.8	121	2	S68145	fibroblast growth	196	6	2.8	199	2	F98312	hypothetical prote
124	6	2.8	124	2	C63729	urease (beta subun	197	6	2.8	200	2	AD3207	transcription regu
125	6	2.8	124	2	E83681	urease beta subuni	198	6	2.8	201	2	AE1880	transposase alr059
126	6	2.8	124	2	H82890	urease complex com	199	6	2.8	202	1	TVMSHS	fibroblast growth
127	6	2.8	129	2	A28302	beta-galactoside-b	200	6	2.8	204	2	S24985	nef protein - huma
128	6	2.8	131	2	D72628	hypothetical prote	201	6	2.8	205	1	ASLJH3	nef protein - huma
129	6	2.8	133	2	D70911	hypothetical prote	202	6	2.8	205	1	ASLJIK	nef protein - siml
130	6	2.8	134	2	B64961	outer membrane por	203	6	2.8	205	2	S43467	nef protein - huma
131	6	2.8	135	2	B63103	translation initia	204	6	2.8	205	2	T35505	hypothetical prote
132	6	2.8	136	2	D90027	urease beta subuni	205	6	2.8	206	1	TVHHS	fibroblast growth
133	6	2.8	141	2	S52446	Ig heavy chain V r	206	6	2.8	206	1	ASLJL2	nef protein - huma
134	6	2.8	141	2	S13836	hemoglobin - sludg	207	6	2.8	206	1	ASLJVL	nef protein - huma
135	6	2.8	142	2	T42849	hypothetical prote	208	6	2.8	206	1	ASLJFV	nef protein - huma
136	6	2.8	143	1	WZBE32	gene 32 protein -	209	6	2.8	206	2	JC4268	fibroblast growth
137	6	2.8	143	1	E70980	hypothetical prote	210	6	2.8	206	2	S03244	nef protein (clone
138	6	2.8	143	2	F71980	hypothetical prote	211	6	2.8	206	2	S03245	nef protein - huma
139	6	2.8	144	2	AB0325	urease (EC 3.5.1.5	212	6	2.8	206	2	S25937	nef protein - huma
140	6	2.8	144	2	H71853	hypothetical prote	213	6	2.8	206	2	S33986	nef protein - huma
141	6	2.8	144	2	H64659	hypothetical prote	214	6	2.8	206	2	S33986	nef protein - huma
142	6	2.8	146	2	H95953	conserved hypothet	215	6	2.8	207	1	QQLJND	nef protein - huma
143	6	2.8	146	2	T28641	Y4JN protein - Rhi	216	6	2.8	208	2	S20102	hypothetical prote
144	6	2.8	146	2	C75212	hypothetical prote	217	6	2.8	208	2	S14192	fibroblast growth
145	6	2.8	149	2	A33353	calcium-binding pr	218	6	2.8	208	2	A86455	hypothetical prote
146	6	2.8	151	2	B64110	arginine repressor	219	6	2.8	210	1	ASLJ02	nef protein - huma
147	6	2.8	151	2	AG2822	conserved hypothet	220	6	2.8	210	2	B60272	hypothetical IgAl
148	6	2.8	152	2	A87679	conserved hypothet	221	6	2.8	211	2	D83327	probable CDP-alcoh
149	6	2.8	152	2	T30112	hypothetical prote	222	6	2.8	212	1	QQLJZR	nef protein - huma
150	6	2.8	153	2	AI2224	hypothetical prote	223	6	2.8	213	2	E64145	hypothetical prote
151	6	2.8	154	2	C72503	hypothetical prote	224	6	2.8	214	1	I44001	nef protein - huma
152	6	2.8	155	2	AG0443	outer membrane lip	225	6	2.8	215	2	G95420	probable oxidoredu
153	6	2.8	155	2	AH3297	hypothetical prote	226	6	2.8	216	2	H87621	DnaJ-related prote
154	6	2.8	156	2	A33888	arginine repressor	227	6	2.8	217	2	T17475	enoyl-coA hydratase
155	6	2.8	156	2	S21802	repressor of arg r	228	6	2.8	218	1	ASLJBR	nef protein - huma
156	6	2.8	156	2	F91142	arginine repressor	229	6	2.8	218	2	B29231	glutathione transf
157	6	2.8	156	2	AF0427	arginine repressor	230	6	2.8	218	2	A39375	glutathione transf
158	6	2.8	156	2	A85988	arginine repressor	231	6	2.8	218	2	S01719	glutathione transf
159	6	2.8	156	2	AE0910	u1 snRNP 70K prote	232	6	2.8	218	2	B28946	glutathione transf
160	6	2.8	156	2	S03047	autoinducer-2 prod	233	6	2.8	219	2	A84182	hypothetical prote
161	6	2.8	160	2	A95040	autoinducer-2 prod	234	6	2.8	220	2	A87056	conserved hypothet
162	6	2.8	160	2	D97910	3-isopropylmalate	235	6	2.8	221	2	A41655	fructokinase (EC 2
163	6	2.8	163	2	A75160	urease (EC 3.5.1.5	236	6	2.8	221	2	H83608	probable transcrip
164	6	2.8	164	1	S31418	hypothetical prote	237	6	2.8	223	2	T21437	hypothetical prote
165	6	2.8	164	2	F87296	hypothetical prote	238	6	2.8	225	2	B84653	TINY-like AP2 doma
166	6	2.8	165	2	F72659	probable 4-hydroxy	239	6	2.8	226	2	H67349	smooth muscle myos
167	6	2.8	166	2	B81981	probable 4-hydroxy	240	6	2.8	226	2	H87436	hypothetical prote
168	6	2.8	166	2	B81036	hypothetical prote	241	6	2.8	227	2	T42015	probable RNA polym
169	6	2.8	167	2	A11129	probable methionin	242	6	2.8	228	2	D75586	urease, beta/gamma
170	6	2.8	168	2	C95392	conserved hypothet	243	6	2.8	228	2	E83614	conserved hypothet
171	6	2.8	170	2	G90157	hypothetical prote	244	6	2.8	228	2	AG3480	25K outer-membrane
172	6	2.8	171	2	D83612	hypothetical prote	245	6	2.8	228	2	A87011	probable TetR-fami
173	6	2.8	173	2	T19290	hypothetical prote	246	6	2.8	228	2	T35738	hypothetical prote
174	6	2.8	174	2	D70979	probable purE prot	247	6	2.8	231	2	JQ1247	hypothetical 25.7K
175	6	2.8	175	2	T33720	hypothetical prote	248	6	2.8	231	2	E98256	hypothetical prote

249	231	2	2.8	6	hypothetical prote	322	6	2.8	281	2	C87073	conserved hypothet
250	231	2	2.8	6	probable sugar-pho	333	6	2.8	282	2	AG3112	hypothetical prote
251	231	2	2.8	6	hypothetical prote	334	6	2.8	282	2	D81089	RplR/YebK/YfhH fam.
252	232	2	2.8	6	G-box-binding prot	335	6	2.8	282	2	T26397	hypothetical prote
253	234	2	2.8	6	nitrate reductase	336	6	2.8	283	2	S52928	XSGU1 protein - Af
254	235	2	2.8	6	C-terminal domain-	337	6	2.8	283	2	S39602	class I histocompa
255	236	2	2.8	6	ubiquitin thiolest	338	6	2.8	283	2	S42393	G-box-binding prot
256	236	2	2.8	6	probable lipoprote	339	6	2.8	284	2	T23158	hypothetical prote
257	236	2	2.8	6	apolipoprotein B m	339	6	2.8	284	2	F98174	oligopeptide ABC t
258	237	1	2.8	6	25K outer-membrane	331	6	2.8	284	2	E70232	hypothetical prote
259	238	2	2.8	6	urease (EC 3.5.1.5	332	6	2.8	284	2	T28887	collagen dpy-10 -
260	238	2	2.8	6	MYB27 protein - Ar	333	6	2.8	284	2	S74256	homeotic protein s
261	238	2	2.8	6	hypothetical prote	334	6	2.8	285	2	S72787	hypothetical prote
262	239	2	2.8	6	cell wall protein	335	6	2.8	285	2	A75629	probable hydrolase
263	239	2	2.8	6	probable manganese	336	6	2.8	285	2	C83254	probable aspartate
264	241	2	2.8	6	respiratory nitrat	337	6	2.8	288	2	T17664	branched-chain ami
265	242	1	2.8	6	DNA repair protein	338	6	2.8	288	2	G64425	pyridoxal kinase (
266	242	2	2.8	6	DNA repair protein	339	6	2.8	288	2	AI0810	probable hydrolase
267	242	2	2.8	6	DNA repair protein	340	6	2.8	291	2	G70605	conserved hypothet
268	242	2	2.8	6	DNA repair protein	341	6	2.8	291	2	AE0298	probable transcrip
269	242	2	2.8	6	hypothetical prote	342	6	2.8	292	2	D83580	hypothetical prote
270	243	2	2.8	6	conserved hypothet	343	6	2.8	293	2	P90978	unknown protein li
271	243	2	2.8	6	ZK688.7 protein -	344	6	2.8	293	2	E86474	serine/threonine-s
272	244	2	2.8	6	NAD---asparagine A	345	6	2.8	294	2	T10690	probable membrane
273	244	2	2.8	6	hypothetical prote	346	6	2.8	294	2	S59774	hypothetical prote
274	246	1	2.8	6	type II site-speci	347	6	2.8	294	2	A90542	hypothetical prote
275	246	2	2.8	6	early auxin-induci	348	6	2.8	295	2	S67919	transcription regu
276	246	2	2.8	6	probable glutamate	349	6	2.8	296	2	A64035	hypothetical prote
277	248	2	2.8	6	hypothetical prote	350	6	2.8	296	2	G84337	methionyl aminopep
278	251	1	2.8	6	probable uridylyate	351	6	2.8	296	2	G90063	hypothetical prote
279	251	2	2.8	6	qEg16 protein -	352	6	2.8	297	2	S01176	hypothetical prote
280	255	1	2.8	6	nef protein - huma	353	6	2.8	298	2	T29297	hypothetical prote
281	255	2	2.8	6	uracil-DNA glycosy	354	6	2.8	300	1	A32566	ubiquinol--cytochr
282	255	2	2.8	6	uracil-DNA glycosy	355	6	2.8	300	2	G89915	conserved hypothet
283	255	2	2.8	6	hypothetical prote	356	6	2.8	301	2	T35805	hypothetical prote
284	257	2	2.8	6	hypothetical prote	357	6	2.8	302	2	AB0510	citg protein limpo
285	257	2	2.8	6	hypothetical prote	358	6	2.8	302	2	F75619	probable hemin ABC
286	257	2	2.8	6	thiosulfate sulfur	359	6	2.8	304	2	B75486	probable snG prot
287	260	1	2.8	6	nef protein - huma	360	6	2.8	304	2	S59965	phosphotransferase
288	261	2	2.8	6	hypothetical 30K P	361	6	2.8	304	2	F84298	hypothetical prote
289	261	2	2.8	6	hypothetical prote	362	6	2.8	306	2	G86593	Yop translocation
290	262	2	2.8	6	4-hydroxy-2-oxoval	363	6	2.8	306	2	C71498	probable yop trans
291	262	2	2.8	6	probable transient	364	6	2.8	306	2	C72030	type III secretion
292	262	2	2.8	6	probable transient	365	6	2.8	306	2	F97600	hypothetical prote
293	263	2	2.8	6	phenylacetic acid	366	6	2.8	307	1	S18524	fructokinase (EC 2
294	264	2	2.8	6	fibroblast growth	367	6	2.8	307	2	AH3374	transporter, dme f
295	264	2	2.8	6	conserved hypothet	368	6	2.8	309	2	JC4958	serine hydroxymeth
296	264	2	2.8	6	an E. coli protein	369	6	2.8	309	2	T31135	hypothetical prote
297	264	2	2.8	6	an E. coli protein	370	6	2.8	310	2	S50696	collagen alpha 1(I
298	265	2	2.8	6	probable lipote-p	371	6	2.8	310	2	G83248	probable permease
299	265	2	2.8	6	hypothetical prote	372	6	2.8	310	2	T50879	phytoene synthase
300	266	2	2.8	6	fibroblast growth	373	6	2.8	312	2	B37245	1-phosphofructokin
301	266	2	2.8	6	nitrate transport	374	6	2.8	312	2	D91011	fructose-1-phospha
302	267	1	2.8	6	fibroblast growth	375	6	2.8	312	2	F85855	fructose-1-phospha
303	267	2	2.8	6	myo-inositol-1(or	376	6	2.8	312	2	AF0158	1-phosphofructokin
304	267	2	2.8	6	hypothetical prote	377	6	2.8	312	2	AE0783	1-phosphofructokin
305	267	2	2.8	6	orotidine-5'-monop	378	6	2.8	313	1	BBSMRP	mannosyl-glycoprot
306	270	2	2.8	6	probable RING zinc	379	6	2.8	313	2	AG4069	1-phosphofructokin
307	272	2	2.8	6	hypothetical prote	380	6	2.8	315	2	AG2012	hypothetical prote
308	272	2	2.8	6	CCAAT box binding	381	6	2.8	316	1	FWYCG	H+-transporting tw
309	273	2	2.8	6	hypothetical prote	382	6	2.8	317	2	I37371	ER calcium-binding
310	273	2	2.8	6	manganese-containi	383	6	2.8	318	2	T44792	2-keto-3-deoxygluc
311	274	2	2.8	6	conserved hypothet	384	6	2.8	318	2	E96033	transcription regu
312	275	2	2.8	6	probable partition	385	6	2.8	318	2	D83330	probable cobW prot
313	276	2	2.8	6	DNA-damage repair	386	6	2.8	320	2	A75278	octaprenyl-diphosp
314	277	1	2.8	6	indole-3-glycerol-	387	6	2.8	322	2	AH0903	homeotic protein H
315	278	2	2.8	6	chromosome partiti	388	6	2.8	323	2	S16318	conserved hypothet
316	278	2	2.8	6	hypothetical prote	389	6	2.8	324	2	E83320	transcription init
317	279	2	2.8	6	probable sugar tra	390	6	2.8	326	2	B69412	hypothetical prote
318	279	2	2.8	6	hypothetical prote	391	6	2.8	326	2	B87557	hypothetical prote
319	280	2	2.8	6	beta-aspartate met	392	6	2.8	326	2	S27534	probable transport
320	280	2	2.8	6	hypothetical prote	393	6	2.8	328	2	G85727	conserved hypothet
321	281	2	2.8	6	probable electron	394	6	2.8	328	2	B87697	

395	6	2.8	328	2	G97017	uncharacterized me	468	2.8	376	2	E70918	hypothetical prote
396	6	2.8	329	2	C97264	UDP-galactose 4-ep	469	2.8	376	2	T39454	hypothetical prote
397	6	2.8	329	2	F95298	aldehyde or keto o	470	2.8	376	2	A96951	TPR-repeat-contain
398	6	2.8	330	2	S74255	homeotic protein s	471	2.8	377	2	S76013	heat shock protein
399	6	2.8	331	2	S50212	bis(9'nucleo) tetr	472	2.8	377	2	G85975	hypothetical prote
400	6	2.8	331	2	A36358	T-cell acute lymph	473	2.8	378	2	S04336	U1 snRNP 70K prote
401	6	2.8	332	2	H83069	probable c4'-dicarb	474	2.8	378	2	C85431	hypothetical prote
402	6	2.8	333	2	B84195	hypothetical prote	475	2.8	379	2	T50751	hydroxyneurosporen
403	6	2.8	333	2	T29242	hypothetical prote	476	2.8	379	2	D70786	probable gcvt prot
404	6	2.8	335	2	B72668	hypothetical prote	477	2.8	379	2	C84577	probable nucleosom
405	6	2.8	337	2	A83216	ABC transporter, m	478	2.8	381	2	G64612	rod shape-determin
406	6	2.8	339	2	T11751	transcription repr	479	2.8	381	2	A64783	ybb2 protein - Esc
407	6	2.8	339	2	C96508	hypothetical prote	480	2.8	381	2	H90700	glycerate kinase I
408	6	2.8	340	2	A64902	peptide transport	481	2.8	381	2	C85551	probable fadE13 pr
409	6	2.8	340	2	A10392	thiamin biosynthes	482	2.8	382	2	E70719	conserved hypotet
410	6	2.8	341	2	A50675	probable alcohol d	483	2.8	383	2	B69232	hypothetical prote
411	6	2.8	341	2	T34693	hypothetical prote	484	2.8	383	2	T26902	acriflavin resista
412	6	2.8	341	2	E83340	hypothetical prote	485	2.8	383	2	AH3457	N-acetyl-galactosam
413	6	2.8	342	2	D75184	probable RNA-3'-ph	486	2.8	384	2	G91130	probable rubredoxi
414	6	2.8	342	2	T22428	hypothetical prote	487	2.8	384	2	G82976	thiolase family pr
415	6	2.8	343	1	D33858	mercury(II) reduct	488	2.8	385	2	S28360	probable oxygen-in
416	6	2.8	344	2	H72213	N utilization subs	489	2.8	387	2	A82014	capsule polysaccha
417	6	2.8	346	1	S35500	heterogeneous ribo	490	2.8	388	2	B89925	chorismate synthas
418	6	2.8	346	2	A45885	MHC class I histoc	491	2.8	389	2	T08128	probable sedoneptu
419	6	2.8	347	2	E95194	D-alanine--D-alani	492	2.8	389	2	T08135	sedoneptulose-bisp
420	6	2.8	347	2	B98061	D-alanine--D-alani	493	2.8	390	1	RRBPT4	recombination/rep
421	6	2.8	348	2	B75312	branched-chain ami	494	2.8	390	2	H87345	thiolase family pr
422	6	2.8	349	2	J02300	replicase - pepper	495	2.8	391	2	G82320	probable oxygen-in
423	6	2.8	349	2	S31875	ALI protein - pepp	496	2.8	391	2	S15220	capsule polysaccha
424	6	2.8	349	2	E89795	conserved hypotet	497	2.8	391	2	AD2501	hypothetical prote
425	6	2.8	351	2	J02327	ALI protein - Indi	498	2.8	391	2	H98138	hypothetical prote
426	6	2.8	352	1	QCCLV1	ALI protein - toma	499	2.8	391	2	AC3149	glycosyltransferas
427	6	2.8	355	1	QCCWV1	AV1 protein - abut	500	2.8	392	2	H83198	probable MFS trans
428	6	2.8	355	2	E83741	hypothetical prote	501	2.8	393	2	T03216	enoyl-lacyl-carrie
429	6	2.8	356	2	F84072	hypothetical prote	502	2.8	393	2	E97761	hypothetical prote
430	6	2.8	357	1	QCCVC1	ALI protein - toma	503	2.8	394	2	B75404	probable amidase -
431	6	2.8	358	1	JQ1870	ALI protein - toma	504	2.8	394	2	T37520	arginase family pr
432	6	2.8	358	2	S44233	strp protein - Str	505	2.8	395	2	H75457	hypothetical prote
433	6	2.8	358	2	I38920	prostaglandin E2 r	506	2.8	397	2	AG0490	probable Arac-fam
434	6	2.8	358	2	S51312	Ep2 prostaglandin	507	2.8	398	2	I56540	protein-tyrosine-p
435	6	2.8	358	2	S07594	hypothetical prote	508	2.8	398	2	G90225	hypothetical prote
436	6	2.8	359	2	S22593	hypothetical prote	509	2.8	398	2	A58922	esterase/N-deacety
437	6	2.8	359	2	S39211	gene C1 protein -	510	2.8	398	2	AE3577	sugar-binding prot
438	6	2.8	359	2	S39235	gene C1 protein -	511	2.8	399	2	A83354	hypothetical prote
439	6	2.8	359	2	T39944	hypothetical trans	512	2.8	401	1	QXBP1L	hypothetical prote
440	6	2.8	360	2	B36470	Wnt-2 protein - mo	513	2.8	401	2	T51493	stearoyl-acyl carr
441	6	2.8	360	2	S00834	int-1-like protein	514	2.8	401	2	T19771	hypothetical prote
442	6	2.8	360	2	AE0172	probable outer mem	515	2.8	402	2	T52356	related to GTP-bin
443	6	2.8	360	2	S59885	replication-associ	516	2.8	403	2	E71300	probable protein-g
444	6	2.8	360	2	H87699	conserved hypotet	517	2.8	404	2	AF3236	thermophilic desul
445	6	2.8	361	1	QCCVPT	ALI protein - pota	518	2.8	405	2	D81918	sodium-translocati
446	6	2.8	361	2	S32168	dimethylallyltrans	519	2.8	405	2	G81184	Na(+)-translocati
447	6	2.8	362	1	JQ1887	ALI protein - toma	520	2.8	406	2	C75537	conserved hypotet
448	6	2.8	362	2	A71243	probable maltose/m	521	2.8	407	1	S65531	sodium-translocati
449	6	2.8	362	2	A75208	sugar transport AT	522	2.8	407	2	E71665	bicyclomycin resis
450	6	2.8	365	1	MMBP2	outer membrane por	523	2.8	407	2	E98347	hypothetical prote
451	6	2.8	365	1	MMECNC	outer membrane por	524	2.8	407	2	AB2935	conserved hypotet
452	6	2.8	365	2	A83727	naringenin-chalcon	525	2.8	408	2	B82094	sodium-translocati
453	6	2.8	366	2	A86837	conserved hypotet	526	2.8	409	2	AG2869	N-carbamoyl-beta-a
454	6	2.8	366	2	AH2429	hypothetical prote	527	2.8	411	1	D64052	Na+-translocating
455	6	2.8	367	2	T44888	probable aminometh	528	2.8	413	2	E84120	serine hydroxymeth
456	6	2.8	367	2	T48692	hypothetical prote	529	2.8	413	2	H83833	hypothetical prote
457	6	2.8	368	2	C69590	chorismate synthas	530	2.8	414	1	H69963	DNA-damage repair
458	6	2.8	369	2	S60063	succinyl-diaminopi	531	2.8	415	2	A97646	n-carbamoyl-beta-a
459	6	2.8	369	2	JQ1974	HTF9-C protein - m	532	2.8	415	2	T00678	hypothetical prote
460	6	2.8	369	2	A75166	hypothetical prote	533	2.8	417	2	E75303	aminopeptidase - D
461	6	2.8	370	2	E71221	hypothetical prote	534	2.8	418	2	E71848	probable nucleosid
462	6	2.8	371	2	S76682	hypothetical prote	535	2.8	418	2	D61667	pyrimidine nucleos
463	6	2.8	372	2	A42778	agglutinin precurs	536	2.8	418	2	S77640	exopolysaccharide
464	6	2.8	373	2	AB1224	cobalamin biosynth	537	2.8	419	2	G71311	probable phosphogl
465	6	2.8	373	2	H84404	ferrichrome ABC tr	538	2.8	419	2	G70652	probable sers prot
466	6	2.8	373	1	G70736	IMP dehydrogenase-	539	2.8	419	2	H95357	probable TtuD3 hyd
467	6	2.8	375	2	H83290	conserved hypotet	540	2.8	419	2	G90264	hypothetical prote

541	6	2.8	422	2	D72302	hypotheical prote	614	6	2.8	469	2	A24450	collagen alpha 2(V
542	6	2.8	425	2	E83023	3-deoxy-D-manno-oc	615	6	2.8	469	2	B87094	probable molecular
543	6	2.8	426	2	C70896	glycine hydroxymet	616	6	2.8	473	2	C64739	yadQ protein - Esc
544	6	2.8	426	2	D87153	serine hydroxymeth	617	6	2.8	473	2	G90648	probable channel t
545	6	2.8	426	2	F83420	ATP-dependent Clp	618	6	2.8	473	2	G85499	probable channel t
546	6	2.8	427	2	C84966	3-phosphoshikimate	619	6	2.8	474	2	T19543	hypotheical prote
547	6	2.8	427	2	E72488	probable tryptopha	620	6	2.8	475	2	T45766	hypotheical prote
548	6	2.8	427	2	AD2603	components of type	621	6	2.8	475	2	G96927	probable Zn-depend
549	6	2.8	428	2	E84192	zinc metalloprotei	622	6	2.8	476	2	B41977	retinoic acid rece
550	6	2.8	428	2	F87038	probable membrane	623	6	2.8	480	2	A40815	transcription fact
551	6	2.8	429	2	A56265	uracil transport p	624	6	2.8	481	2	S56299	hypotheical prote
552	6	2.8	429	2	G91048	uracil transport E	625	6	2.8	482	2	E96985	altronate oxidore
553	6	2.8	429	2	C85893	uracil transport I	626	6	2.8	482	2	S76475	hypotheical prote
554	6	2.8	429	2	AG0818	uracil permease (u	627	6	2.8	483	2	H87492	yJef family protei
555	6	2.8	429	2	C87580	Xaa-Pro dipeptidas	628	6	2.8	483	2	T36811	probable integral
556	6	2.8	431	2	T07685	omega-3 fatty acid	629	6	2.8	483	2	AC0913	sodium/pantothena
557	6	2.8	431	2	G83404	probable chemotaxi	630	6	2.8	484	1	A46217	GPI-anchor biosynt
558	6	2.8	431	2	J50055	hypotheical 43.7K	631	6	2.8	484	2	A86503	pyruvate kinase I
559	6	2.8	432	2	S38893	uracil transport p	632	6	2.8	484	2	A72119	pyruvate kinase CP
560	6	2.8	432	2	T24072	hypotheical prote	633	6	2.8	484	2	H64105	pantothenate trans
561	6	2.8	433	2	H70141	enolase (eno) homo	634	6	2.8	484	2	AB0445	sodium/pantothena
562	6	2.8	433	2	A70536	probable pepC prot	635	6	2.8	485	1	A55731	GPI-anchor biosynt
563	6	2.8	434	2	A57986	membrane-bound ura	636	6	2.8	485	2	I52484	gene FIG-A protein
564	6	2.8	434	2	F90184	cobyrinic acid A,C	637	6	2.8	485	2	D65118	pantothenate perme
565	6	2.8	435	2	E86266	protein F3F19.23 I	638	6	2.8	485	2	B91145	sodium/pantothena
566	6	2.8	436	2	F82422	anaerobic glycerol	639	6	2.8	485	2	F85990	sodium/pantothena
567	6	2.8	438	2	H71674	proline/betaine tr	640	6	2.8	486	2	S76523	serine-type D-Ala-
568	6	2.8	438	2	A72430	hypotheical prote	641	6	2.8	486	2	D70439	conserved hypotet
569	6	2.8	438	2	S3787	collagen alpha cha	642	6	2.8	489	2	H86711	4-alpha-glucanotr
570	6	2.8	438	2	F81659	D-alanyl-D-alanine	643	6	2.8	490	2	B86265	cytochrome P450 7I
571	6	2.8	439	2	D83345	L-sorbose dehydr	644	6	2.8	491	2	S48827	1-aminocyclopropan
572	6	2.8	440	2	I50213	protein-tyrosine-p	645	6	2.8	492	2	S61242	virion serine/thre
573	6	2.8	440	2	C84832	probable methionyl	646	6	2.8	495	2	T13019	1-aminocyclopropan
574	6	2.8	440	2	C82410	conserved hypotet	647	6	2.8	495	2	G95147	polysaccharide bio
575	6	2.8	441	2	C87233	probable cell inva	648	6	2.8	495	2	T05388	hypotheical prote
576	6	2.8	441	2	E90051	hypotheical prote	649	6	2.8	495	2	E98015	conserved hypotet
577	6	2.8	442	2	A83122	probable MFS trans	650	6	2.8	496	2	AI0907	probable sialic ac
578	6	2.8	442	2	G86294	T24D18.11 protein	651	6	2.8	498	2	C83717	NADP-dependent ald
579	6	2.8	442	2	A12272	hypotheical prote	652	6	2.8	500	2	A41552	aldosterone syntha
580	6	2.8	443	2	H87185	aminopeptidase I	653	6	2.8	500	2	E87009	probable two-compo
581	6	2.8	444	2	T20374	hypotheical prote	654	6	2.8	501	2	A38650	myosin heavy chain
582	6	2.8	445	2	T49556	epithelial zinc-fi	655	6	2.8	501	2	T36051	probable cytochrom
583	6	2.8	446	2	T17018	1-aminocyclopropan	656	6	2.8	501	2	E70596	hypotheical prote
584	6	2.8	446	2	C81058	hypotheical prote	657	6	2.8	503	2	T38997	vacuolar atp synth
585	6	2.8	446	2	A83355	hypotheical prote	658	6	2.8	503	2	S25335	H+-transporting AT
586	6	2.8	446	2	H85076	probable athila tr	659	6	2.8	503	2	D70926	hypotheical prote
587	6	2.8	447	2	F82619	proton glutamate s	660	6	2.8	503	2	D98116	hypotheical prote
588	6	2.8	449	2	I39489	L-sorbose dehydr	661	6	2.8	503	2	G95251	conserved hypotet
589	6	2.8	450	2	G01158	tyrosine kinase ac	662	6	2.8	504	2	JC1306	virion protein hom
590	6	2.8	451	2	D84091	hypotheical prote	663	6	2.8	504	2	G02474	interferon regulat
591	6	2.8	452	2	B90407	conserved hypotet	664	6	2.8	504	2	H87672	conserved hypotet
592	6	2.8	452	2	H75379	conserved hypotet	665	6	2.8	505	2	T46996	hypotheical prote
593	6	2.8	454	2	D70904	probable mcal prot	666	6	2.8	505	2	AG0239	succinylglutamic s
594	6	2.8	456	2	T06589	3-methyl-2-oxobuta	667	6	2.8	505	2	G70954	probable lyss prot
595	6	2.8	456	2	T40367	n-acetylglucosamin	668	6	2.8	505	2	C53153	glucose transport
596	6	2.8	456	2	T39014	hypotheical zinc-	669	6	2.8	505	2	AC3361	GTP-binding protei
597	6	2.8	457	2	S03961	Ig mu chain C regi	670	6	2.8	506	2	B65114	probable sialic ac
598	6	2.8	459	2	A75097	hypotheical prote	671	6	2.8	506	2	A91141	sialic acid transp
599	6	2.8	459	2	T21167	hypotheical prote	672	6	2.8	506	2	D85986	hypotheical prote
600	6	2.8	460	2	H87396	conserved hypotet	673	6	2.8	506	2	S65193	H+-transporting tw
601	6	2.8	461	2	A31237	alpha-2C-adrenergi	674	6	2.8	508	1	PKWA	glycerol-3-phospha
602	6	2.8	462	1	A41326	enantiomer-selecti	675	6	2.8	508	2	T22440	hypotheical prote
603	6	2.8	462	2	D32057	nitrogenase (EC 1.	676	6	2.8	510	2	A55207	glycerol-3-phospha
604	6	2.8	462	2	D97385	cpaE protein (AF22	677	6	2.8	510	2	AH0366	probable sugar tra
605	6	2.8	463	2	C70931	probable PPE prote	678	6	2.8	510	2	H87320	conserved hypotet
606	6	2.8	464	2	B81817	probable integral	679	6	2.8	512	2	B83197	glycerol-3-phospha
607	6	2.8	464	2	B55223	major tail protein	680	6	2.8	512	2	A54400	protein kinase (EC
608	6	2.8	465	1	WMBE28	UL38 protein - hum	681	6	2.8	513	2	A99839	Na+/H+ antiporter
609	6	2.8	465	1	WMBE44	maturatation protei	682	6	2.8	513	2	G64864	Na+/H+-exchanging
610	6	2.8	465	2	G95973	endo-1,3-l,4-beta-	683	6	2.8	513	2	A85897	Na+/H+ antiporter,
611	6	2.8	466	1	WMBE71	capsid protein ICP	684	6	2.8	513	2	AD3505	7.5K chlorosome pr
612	6	2.8	466	2	A95355	probable inner-mem	685	6	2.8	514	2	AG0723	regulator of intra
613	6	2.8	467	2	T10879	y41C protein - Rhi	686	6	2.8	515	2	A70905	hypotheical prote

587 516 1 JC1172 histidine ammonia-
588 516 2 JE0301 inulinase (EC 3.2.
589 516 2 H71332 hypothetical prote
590 519 2 T07026 ethylene receptor
591 520 2 C87450 GMP synthase [lipo
592 523 2 T20828 hypothetical prote
593 527 2 AD1346 propionate CoA-tra
594 527 2 AG1716 propionate CoA-tra
595 528 2 JC4814 Na+/H+-exchanging
596 530 2 G70904 hypothetical prote
597 530 2 C82144 Na+/H+ antiporter
598 531 2 D70946 NADH dehydrogenase
599 531 2 T35226 nitrate reductase
600 532 2 D69281 CTP synthase (pyrG
601 532 1 A33813 sterol 26-monooxyg
602 535 2 C95057 CTP synthase [lipo
603 535 2 F97925 CTP synthase (EC 6
604 535 2 S74703 hypothetical prote
605 537 2 T28683 hypothetical prote
606 538 2 F83622 probable permease
607 539 2 D96562 unknown protein [i
608 540 2 E71503 probable adp/atr t
609 545 2 B70374 conserved hypothet
610 545 2 G90420 threonyl-tRNA synt
611 547 2 T06758 probable galactose
612 555 2 C96667 unknown protein, 7
613 556 2 S22634 sphingomyelin phos
614 557 2 B28182 hemolysin B - Serr
615 558 2 B82984 hypothetical prote
616 559 2 AH1719 pheromone ABC tran
617 562 2 S44464 probable membrane
618 563 2 AC2923 conserved hypothet
619 563 2 G97697 hypothetical prote
620 564 2 E98291 probable 3,4-dihyd
621 564 2 AE2992 3,4-dihydroxy-2-bu
622 564 2 H06278 F14L17.20 protein
623 569 2 S47277 gp88 protein - mur
624 570 2 C98885 DNA-dependent DNA
625 572 2 F90297 ATP-dependent RNA
626 576 1 NDBSR1 type II site-speci
627 576 2 C87261 hypothetical prote
628 576 2 T18067 hypothetical prote
629 577 2 T40297 membrane transport
630 580 2 T45022 transducer-like pr
631 581 1 F70423 DNA polymerase bet
632 582 2 A57068 protein-tyrosine-p
633 586 2 T52148 transport protein
634 589 1 R8BPBQ RNA-directed RNA p
635 589 2 T05074 hypothetical prote
636 589 2 A71918 probable secretion
637 591 2 G90989 probable chaperoni
638 592 2 B83231 probable short-cha
639 592 2 D75421 conserved hypothet
640 593 2 F95939 probable adenine d
641 593 2 H64594 multidrug resistan
642 595 2 A48658 flagellin - Escher
643 595 2 B48658 flagellin - Escher
644 598 2 S55638 minor capsid prote
645 600 2 D90155 hypothetical prote
646 601 2 T04747 hypothetical prote
647 604 2 S57065 probable membrane
648 604 2 F72035 conserved hypothet
649 604 2 F86589 CF589 hypothetical
650 607 2 JQ1132 phenol 2-monooxyge
651 611 2 G83177 probable sodium/hy
652 613 2 JC7762 SOX-3 protein - qu
653 614 2 B82329 sulfite reductase
654 614 2 A25707 U1 snRNP 70K prote
655 616 2 C83447 conserved hypothet
656 617 2 S75447 proline-tRNA ligas
657 617 2 JC4559 methylmalonyl-CoA
658 617 2 F75484 hypothetical prote
659 618 2 JC4366 transcription fact

760 6 2.8 619 2 AI3336 potassium/proton a
761 6 2.8 620 2 S48772 AFRI protein - yea
762 6 2.8 621 2 S10450 myosin heavy chain
763 6 2.8 625 2 D83753 PTS system, fructo
764 6 2.8 625 2 D86244 protein Ser/Thr pr
765 6 2.8 627 2 T47968 dynamin-like prote
766 6 2.8 628 2 T08942 proton pump intera
767 6 2.8 629 2 G84481 probable receptor-
768 6 2.8 629 2 T34726 probable dehydroge
769 6 2.8 632 2 B83163 probable AMP-bindi
770 6 2.8 634 2 T36614 hypothetical prote
771 6 2.8 635 2 H69626 PTS fructose-speci
772 6 2.8 635 2 T07794 ethylene receptor
773 6 2.8 636 2 S41067 collagen alpha 1(I
774 6 2.8 637 2 B81939 probable threonine
775 6 2.8 637 2 E81167 threonyl-tRNA synt
776 6 2.8 644 2 JC5119 anti-mullerian hor
777 6 2.8 645 2 A75533 conserved hypothet
778 6 2.8 646 2 A85834 probable chaperoni
779 6 2.8 648 2 T45575 hypothetical prote
780 6 2.8 650 2 T21498 hypothetical prote
781 6 2.8 651 2 B96665 protein F22C12.22
782 6 2.8 652 2 A37000 leukemia virus rec
783 6 2.8 652 2 I48083 amphotropic murine
784 6 2.8 653 2 D69815 conserved hypothet
785 6 2.8 654 2 A96235 hydroxamate-depend
786 6 2.8 654 2 AC3051 hypothetical prote
787 6 2.8 655 2 T15879 hypothetical prote
788 6 2.8 655 2 S54183 acyl-CoA dehydroge
789 6 2.8 656 2 S73313 hypothetical prote
790 6 2.8 656 2 A49579 amphotropic murine
791 6 2.8 660 2 B70662 probable membranep
792 6 2.8 660 2 E98169 serine proteinase
793 6 2.8 660 2 AB3118 serine proteinase
794 6 2.8 662 2 T20570 hypothetical prote
795 6 2.8 662 2 A33481 interferon-induced
796 6 2.8 662 2 I37892 IL12 receptor comp
797 6 2.8 666 2 S56781 hypothetical prote
798 6 2.8 669 2 D64137 bett protein homol
799 6 2.8 670 2 T10666 hypothetical prote
800 6 2.8 672 2 S52673 probable membrane
801 6 2.8 674 2 F81990 NADH dehydrogenase
802 6 2.8 674 2 D81220 NADH dehydrogenase
803 6 2.8 674 2 T15524 hypothetical prote
804 6 2.8 674 2 S61181 hypothetical prote
805 6 2.8 680 2 T45736 hypothetical prote
806 6 2.8 682 2 T36877 probable regulator
807 6 2.8 682 2 T18847 hypothetical prote
808 6 2.8 690 2 D75487 v-type ATP synthas
809 6 2.8 692 2 A36143 phospholipase C (E
810 6 2.8 692 2 E83230 non-hemolytic phos
811 6 2.8 695 2 E70923 hypothetical prote
812 6 2.8 698 2 S52696 myosin heavy chain
813 6 2.8 698 2 T17261 hypothetical prote
814 6 2.8 702 2 C71269 probable polyribon
815 6 2.8 702 2 S12638 transposition prot
816 6 2.8 704 1 S50448 1,4-alpha-glucan b
817 6 2.8 710 2 G82689 mitochondrial inte
818 6 2.8 710 2 C70506 soluble lytic mure
819 6 2.8 711 2 C70506 probable fadE34 pr
820 6 2.8 712 2 T18195 gag protein - silk
821 6 2.8 713 2 F82822 NADH-ubiquinone ox
822 6 2.8 714 2 G75623 hypothetical prote
823 6 2.8 715 2 S52675 probable membrane
824 6 2.8 716 2 G83612 hypothetical prote
825 6 2.8 718 2 G70978 probable copper-tr
826 6 2.8 718 2 T05850 homeobox protein A
827 6 2.8 719 2 T02154 protein kinase hom
828 6 2.8 723 2 G84507 hypothetical prote
829 6 2.8 725 2 T00492 hypothetical prote
830 6 2.8 727 2 T18600 hypothetical prote
831 6 2.8 727 2 AD1868 hypothetical prote
832 6 2.8 731 2 I60729 ornithine decarbox

833	6	2.8	731	2	A98109	ornithine decarbox	906	6	2.8	898	2	D86122	Mg2+ transport ATP
834	6	2.8	731	2	D85954	ornithine decarbox	907	6	2.8	902	2	B57147	Mg2+-transporting
835	6	2.8	732	2	A40839	ornithine decarbox	908	6	2.8	902	2	AH1058	Mg(2+) transport A
836	6	2.8	732	2	A99719	ornithine decarbox	909	6	2.8	904	2	AH2019	hypothetical prote
837	6	2.8	732	2	A85569	ornithine decarbox	910	6	2.8	908	2	C70168	DNA polymerase I (
838	6	2.8	740	1	F0LJHD	gag polyprotein -	911	6	2.8	908	2	A83424	assimilatory nitra
839	6	2.8	741	2	D95966	probable aldehyde	912	6	2.8	911	2	T01353	probable serine/th
840	6	2.8	748	2	S59327	hypothetical prote	913	6	2.8	911	2	H70553	penicillin-binding
841	6	2.8	749	2	A70812	hypothetical glyci	914	6	2.8	912	2	D72644	hypothetical prote
842	6	2.8	757	2	S27762	Sip1 protein - bar	915	6	2.8	922	2	I37292	DNA ligase (ATP) (
843	6	2.8	759	2	A82052	two-component hybr	916	6	2.8	924	2	D81349	nitrate reductase
844	6	2.8	763	2	AC0108	probable primase Y	917	6	2.8	924	2	C83572	organic solvent to
845	6	2.8	765	2	S45033	probable imbibitio	918	6	2.8	931	2	S66574	transferrin-bindin
846	6	2.8	765	2	AF0118	probable kinase YP	919	6	2.8	932	1	VBEBEC	glycoprotein g1 pr
847	6	2.8	767	2	E70895	hypothetical glyci	920	6	2.8	932	2	I52527	PACE4A - mouse (fr
848	6	2.8	768	2	S71477	homeotic protein,	921	6	2.8	932	2	T28820	hypothetical prote
849	6	2.8	768	2	H82367	sensory box/GGDPF	922	6	2.8	937	2	I53282	gene PACE4 protein
850	6	2.8	773	2	T46188	inhibition protein	923	6	2.8	940	2	S49087	lactoferrin-bindin
851	6	2.8	779	2	S57805	aconitate hydratase	924	6	2.8	943	2	G81070	lactoferrin-bindin
852	6	2.8	779	2	T21021	hypothetical prote	925	6	2.8	944	2	C81798	lactoferrin bindin
853	6	2.8	781	2	A43866	neuraminidase - Vi	926	6	2.8	944	2	T18911	hypothetical prote
854	6	2.8	782	2	H95306	probable amino aci	927	6	2.8	948	2	C83060	hypothetical prote
855	6	2.8	783	2	A48998	nucleolar protein	928	6	2.8	950	1	S69704	hypothetical prote
856	6	2.8	784	2	E72515	probable DNA-direc	929	6	2.8	952	2	S64473	translation initia
857	6	2.8	787	2	A75347	GTP pyrophosphokin	930	6	2.8	953	2	S19427	probable membrane
858	6	2.8	788	2	C84616	similar to mammali	931	6	2.8	961	2	T23395	hypothetical prote
859	6	2.8	790	1	TVH0TT	nerve growth facto	932	6	2.8	971	2	T32883	hypothetical prote
860	6	2.8	794	2	E90803	hypothetical prote	933	6	2.8	990	2	H86293	protein t24D18.4 [
861	6	2.8	795	2	A85612	hypothetical prote	934	6	2.8	993	2	S46779	26S proteasome reg
862	6	2.8	799	1	TVRTTB	nerve growth facto	935	6	2.8	994	2	A70776	probable glnE - My
863	6	2.8	799	2	C86287	F9L1.24 protein -	936	6	2.8	996	2	F86410	protein F3M18.12 [
864	6	2.8	802	1	A44223	DNA excision repai	937	6	2.8	1001	2	AG1979	hypothetical prote
865	6	2.8	802	2	A83125	probable TonB-depe	938	6	2.8	1013	2	A69226	type I restriction
866	6	2.8	803	2	I68600	dipeptidyl aminope	939	6	2.8	1014	2	AC1971	valyl-tRNA synthet
867	6	2.8	803	2	A41793	dipeptidyl aminope	940	6	2.8	1018	2	H83135	probable adhesin P
868	6	2.8	806	2	A41341	microbial serine p	941	6	2.8	1032	2	H87470	AcrrB/AcrB/AcrF fam
869	6	2.8	807	2	E82158	neuraminidase VC17	942	6	2.8	1043	2	H83329	probable RND efflu
870	6	2.8	812	2	AE3010	TonB-dependent rec	943	6	2.8	1044	2	F95375	probable drug resi
871	6	2.8	815	2	T00546	serine/threonine-s	944	6	2.8	1049	1	CG8078	collagen alpha 1(I
872	6	2.8	817	2	T22442	hypothetical prote	945	6	2.8	1050	2	JC7578	endo-1,4-beta-xyla
873	6	2.8	819	2	B47057	hypothetical kinase (946	6	2.8	1051	2	A38373	ubiquitin--protein
874	6	2.8	819	2	AH0056	aspartate kinase (947	6	2.8	1057	2	A42109	glycine dehydrogen
875	6	2.8	822	2	S19947	fibroblast growth	948	6	2.8	1076	1	A35622	nuclear pore prote
876	6	2.8	822	2	B49151	fibroblast growth	949	6	2.8	1077	2	B82566	acriflavin resista
877	6	2.8	824	2	F87330	photosynthesis pro	950	6	2.8	1083	2	A38919	hypothetical prote
878	6	2.8	825	2	A26983	regulatory protein	951	6	2.8	1089	2	S53978	PSE1 protein - yea
879	6	2.8	830	2	T18860	hypothetical prote	952	6	2.8	1091	2	T34107	hypothetical prote
880	6	2.8	831	2	A48489	nitrate reductase	953	6	2.8	1096	1	S61917	protein kinase C (
881	6	2.8	831	2	S50163	nitrate reductase	954	6	2.8	1099	2	A59311	myosin VIII, 2MK3
882	6	2.8	832	2	A31246	neurogenic protein	955	6	2.8	1116	2	B88612	protein Y76A2A.2 [
883	6	2.8	833	2	S19087	gene Delta protein	956	6	2.8	1117	2	C91286	hypothetical prote
884	6	2.8	833	2	A96274	probable tonB-depe	957	6	2.8	1117	2	G86127	hypothetical prote
885	6	2.8	834	2	A97178	probable permease	958	6	2.8	1131	2	A23944	chitin synthase (E
886	6	2.8	835	2	F72624	probable cation-tr	959	6	2.8	1133	2	T01920	probable RNA-direc
887	6	2.8	838	2	S23606	potassium channel	960	6	2.8	1147	1	MWAXIB	myosin heavy chain
888	6	2.8	839	2	A56337	glycoprotein phosp	961	6	2.8	1154	2	T48829	related to SREBP C
889	6	2.8	841	2	F81172	DNA ligase NMB0666	962	6	2.8	1155	2	G96539	hypothetical prote
890	6	2.8	843	2	B85429	beta-galactosidase	963	6	2.8	1156	2	T14899	aminophospholipid
891	6	2.8	853	2	T04600	probable beta-gala	964	6	2.8	1166	1	S06142	protein-tyrosine k
892	6	2.8	855	2	A48168	proliferating-cell	965	6	2.8	1166	2	S33812	myosin-like protei
893	6	2.8	857	2	S62694	potassium channel	966	6	2.8	1166	2	T13958	myosin-b1 protein
894	6	2.8	862	2	A96778	hypothetical prote	967	6	2.8	1174	1	H3BYDH	helicase (EC 3.6.1
895	6	2.8	865	2	I54331	dipeptidyl aminope	968	6	2.8	1179	2	H82706	hypothetical prote
896	6	2.8	880	2	S00670	neurogenic repetit	969	6	2.8	1181	2	A43346	1-phosphatidylinos
897	6	2.8	886	2	I50694	collagen alpha 1(I	970	6	2.8	1186	2	S61647	probable membrane
898	6	2.8	886	2	S07132	hypothetical prote	971	6	2.8	1187	2	T20544	hypothetical prote
899	6	2.8	889	2	A35989	modulation protein	972	6	2.8	1196	2	S40908	tyB protein - yea
900	6	2.8	891	2	B82495	probable NADH dehy	973	6	2.8	1207	2	T16011	hypothetical prote
901	6	2.8	892	2	T09193	ataxin 7 - human	974	6	2.8	1213	2	T19835	hypothetical prote
902	6	2.8	893	2	T35014	probable regulator	975	6	2.8	1228	2	AE2397	protoporphyrin IX
903	6	2.8	894	2	B96557	probable receptor	976	6	2.8	1231	2	C84716	hypothetical prote
904	6	2.8	898	2	B65236	Mg(2+) transport A	977	6	2.8	1237	2	T14633	hypothetical prote
905	6	2.8	898	2	C91281	Mg2+ transport ATP	978	6	2.8	1238	1	JC5573	copper-transportin

C2H2 type zinc fin
probable non-ribos
Kas-GPase activat
hypothetical prote
neural cell adhesi
probable ATP-depen
TyB protein - years
leucocyte common a
ras GPase-activat
DNA-binding protei
ro-3 protein - Neu
TyB protein - years
TyB protein - years
TyB protein - years
TyB protein - years
1,3-beta-D-glucan-
hypothetical prote
probable membrane
probable retroelem
hypothetical prote
FIM protein (impor

979 6 2.8 1238 2 T40120
980 6 2.8 1249 2 C83358
981 6 2.8 1249 2 T14270
982 6 2.8 1263 2 T00649
983 6 2.8 1265 1 A73967
984 6 2.8 1273 2 E72611
985 6 2.8 1278 2 B22671
986 6 2.8 1290 2 A56493
987 6 2.8 1293 2 T14259
988 6 2.8 1298 2 T47523
989 6 2.8 1300 2 T18364
990 6 2.8 1328 2 S52481
991 6 2.8 1328 2 S52894
992 6 2.8 1328 2 S50948
993 6 2.8 1328 2 B22999
994 6 2.8 1328 2 B28097
995 6 2.8 1339 2 A55301
996 6 2.8 1339 2 G84764
997 6 2.8 1341 2 S66835
998 6 2.8 1356 2 F84486
999 6 2.8 1356 2 T18754
1000 6 2.8 1379 2 T45119

ALIGNMENTS

RESULT 1
JC7353
fibroblast growth factor-20 - human
C:Species: Homo sapiens (man)
C:Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 01-Dec-2000
C:Accession: JC7353
R:Kirkoshi, H.; Sagara, N.; Saitoh, T.; Tanaka, K.; Sekihara, H.; Shiohara, K.; Katoh,
Biochem. Biophys. Res. Commun. 274, 337-343, 2000
A:Title: Molecular cloning and characterization of human FGF-20 on chromosome 8p21.3-p22
A:Reference number: JC7353
A:Accession: JC7353
A:Molecule type: mRNA
A:Residues: 1-211 <KIR>
A:Cross-references: DDBJ:AB044277
C:Comment: This factor is involved in physiological and pathological processes, playing
C:Genetics:
A:Gene: fgf-20
A:Map position: 8p21.3-8p22
C:Superfamily: fibroblast growth factor
C:Keywords: angiogenesis; carcinogenesis

Query Match 100.0%; Score 211; DB 2; Length 211;
Best Local Similarity 100.0%; Pred. No. 1.7e-213;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAPLAEVGGFLGGLEGGLQQVGSFHLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60
Db 1 MAPLAEVGGFLGGLEGGLQQVGSFHLPPAGERPPLLGERRSAERSARGGPGAAQLAHL 60

Qy 61 HGIILRRQLYCRGTGFHLQILPDGVSQGTRODHSILFGLFISVAVGLVSRGVDGSLYL 120
Db 61 HGIILRRQLYCRGTGFHLQILPDGVSQGTRODHSILFGLFISVAVGLVSRGVDGSLYL 120

Qy 121 MNDKGYLGSSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTTPRDGAR 180
Db 121 MNDKGYLGSSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTTPRDGAR 180

Qy 181 SKRHKQKTHFLPRVDPVDPVPELYKDLLMYT 211
Db 181 SKRHKQKTHFLPRVDPVDPVPELYKDLLMYT 211

RESULT 2
JC7511
fibroblast growth factor-20 - rat
C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
C:Accession: JC7511
R:Ohmachi, S.; Watanabe, Y.; Mikami, T.; Kusu, N.; Ibi, T.; Akaike, A.; Itoh, N.
Biochem. Biophys. Res. Commun. 277, 355-360, 2000
A:Title: FGF-20, a novel neurotrophic factor, preferentially expressed in the substan
A:Reference number: JC7511; MUID:20490008
A:Contents: Brain
A:Accession: JC7511
A:Molecule type: DNA
A:Residues: 1-212 <OHM>
A:Cross-references: DDBJ:AB020021
C:Comment: This factor is secreted, and plays an important role as a neurotrophic fac
C:Genetics:
A:Gene: fgf-20
C:Keywords: brain; growth factor; neurotrophic factor

Query Match 40.3%; Score 85; DB 2; Length 212;
Best Local Similarity 100.0%; Pred. No. 3.5e-81;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 124 KGELYGSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTTPRDGARSKR 183
Db 124 KGELYGSEKLTSECFRQFEENWNTYSSNIYKHGDTGRRYFVALNKDGTTPRDGARSKR 183

Qy 184 HQKFTHTFLPRVDPVDPVPELYKDLL 208
Db 184 HQKFTHTFLPRVDPVDPVPELYKDLL 208

RESULT 3
JC7082
fibroblast somatotropin-20 - African clawed frog
N:Alternate names: fibroblast growth factor-20
C:Species: Xenopus laevis (African clawed frog)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: JC7082
R:Koga, C.; Adati, N.; Nakata, K.; Mikoshiba, K.; Furuhata, Y.; Sato, S.; Tei, H.; Sa
Biochem. Biophys. Res. Commun. 261, 756-765, 1999
A:Title: Characterization of a novel member of the FGF family, XFGF-20, in Xenopus la
A:Reference number: JC7082; MUID:99373151
A:Accession: JC7082
A:Molecule type: mRNA
A:Residues: 1-208 <KOG>
A:Cross-references: DDBJ:AB012615; NID:g5762261; PIDN:BAA83474.1; PID:g5762262
C:Superfamily: fibroblast growth factor
C:Keywords: differentiation; fibroblast; growth factor; heparin binding

Query Match 12.3%; Score 26; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.1e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 129 GSEKLTSECFRQFEENWNTYSSN 154
Db 126 GSEKLTSECFRQFEENWNTYSSN 151

RESULT 4
S66486
fibroblast growth factor 9 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S66486
R:Seo, M.; Noguchi, K.
FEBS Lett. 370, 231-235, 1995
A:Title: Retinoic acid induces gene expression of fibroblast growth factor-9 during i
A:Reference number: S66486; MUID:95385801
A:Accession: S66486
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <SEO>
A:Cross-references: EMBL:D38258; NID:g1107458; PIDN:BAA07410.1; PID:g1107459
C:Superfamily: fibroblast growth factor

```
Query Match          9.0%; Score 19; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVIRGVDSGLYLGMN 122
    |||||
Db 101 AVGLVIRGVDSGLYLGMN 119
    |||||

RESULT 5
A48137
fibroblast growth factor 9 - human
N:Alternate names: glia-activating factor
C:Species: Homo sapiens (man)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000
C:Accession: A48137
R: Miyamoto, M.; Naruo, K.; Seko, C.; Matsumoto, S.; Kondo, T.; Kurokawa, T.
Mol. Cell. Biol. 13, 4251-4259, 1993
A: Title: Molecular cloning of a novel cytokine cDNA encoding the ninth member of the fibroblast growth factor family
A: Reference number: A48137; MUID: 93309459
A: Accession: A48137
A: Status: preliminary
A: Molecule type: nucleic acid
A: Residues: 1-208 <MY>
A: Cross-references: GB: D14836; NID: g391718; PIDN: BAA03572.1; PID: g391719
A: Experimental source: foreskin
A: Note: sequence extracted from NCBI backbone (NCBIN:134640, NCBI:134641)
C: Genetics:
A: Gene: GDB: FGF9
A: Cross-references: GDB: 207221; OMIM: 600921
A: Map position: 13q11-13q12
C: Superfamily: fibroblast growth factor

Query Match          9.0%; Score 19; DB 2; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.9e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVIRGVDSGLYLGMN 122
    |||||
Db 101 AVGLVIRGVDSGLYLGMN 119
    |||||

RESULT 6
JC5940
fibroblast growth factor 16 - rat
C: Species: Rattus norvegicus (Norway rat)
C: Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C: Accession: JC5940
R: Miyake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami,
Biochem. Biophys. Res. Commun. 243, 148-152, 1998
A: Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor family
A: Reference number: JC5940; MUID: 98139883
A: Accession: JC5940
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-207 <MY>
A: Cross-references: DBDJ: AB002561; NID: g29111149; PIDN: BAA24947.1; PID: g2911150
C: Superfamily: fibroblast growth factor

Query Match          7.6%; Score 16; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLQYCRGTGFLH 77
    |||||
Db 58 GILRRRLQYCRGTGFLH 73
    |||||

RESULT 7
JC5941
fibroblast growth factor 16 - human
C: Species: Homo sapiens (man)
C: Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
```

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C: Accession: JC5941
R: Miyake, A.; Konishi, M.; Martin, F.H.; Hernday, N.A.; Ozaki, K.; Yamamoto, S.; Mikami,
Biochem. Biophys. Res. Commun. 243, 148-152, 1998
A: Title: Structure and expression of a novel member, FGF-16, of the fibroblast growth factor family
A: Reference number: JC5940; MUID: 98139883
A: Accession: JC5941
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-207 <MY>
A: Cross-references: DBDJ: AB009391; NID: g29111169; PIDN: BAA24956.1; PID: g2911170
C: Superfamily: fibroblast growth factor

Query Match          7.6%; Score 16; DB 2; Length 207;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLQYCRGTGFLH 77
    |||||
Db 58 GILRRRLQYCRGTGFLH 73
    |||||

RESULT 8
E69134
conserved hypothetical protein MTH273 - Methanobacterium thermoautotrophicum (strain
C: Species: Methanobacterium thermoautotrophicum
C: Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Sep-1999
C: Accession: E69134
R: Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
et al.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani,
K.; Liu, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A: Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu
A: Reference number: A69000; MUID: 98037514
A: Accession: E69134
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-151 <MTH>
A: Cross-references: GB: AE000813; GB: AE000666; NID: g2621320; PIDN: AAB84779.1; PID: g262
A: Experimental source: strain Delta H
C: Genetics:
A: Gene: MTH273
C: Superfamily: conserved hypothetical protein ybhB

Query Match          3.8%; Score 8; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LPDGSVQG 87
    |||||
Db 80 LPDGSVQG 87
    |||||

RESULT 9
G87417
conserved hypothetical protein CC1358 [imported] - Caulobacter crescentus
C: Species: Caulobacter crescentus
C: Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C: Accession: G87417
R: Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A: Title: Complete Genome Sequence of Caulobacter crescentus.
A: Reference number: AB7249; MUID: 21173698; PMID: 11259647
A: Accession: G87417
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-157 <STO>
A: Cross-references: GB: AE005673; NID: g13422709; PIDN: AAK23339.1; GSPDB: GN00148
C: Genetics:
A: Gene: CC1358
C: Superfamily: conserved hypothetical protein HI0943
```

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Query Match          3.8%; Score 8; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 RPVDPERV 200
Db 77 RPVDPERV 84

RESULT 10
A86430
F26G16.12 protein - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
C:Accession: A86430
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: A86430
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-197 <STO>
A:Cross-references: GB:AE005172; NID:g6634774; PIDN:AAF19754.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match          3.8%; Score 8; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
Db 117 HGILRRRQ 124

RESULT 11
T01363
hypothetical protein At2g34720 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein T29F13.7
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
C:Accession: T01363; B84760
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A:Reference number: 214179
A:Accession: T01363
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-226 <ROU>
A:Cross-references: EMBL:AC003096; NID:g3132469; PID:g3132473
A:Experimental source: cultivar Columbia
A:Note: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: B84760
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-226 <STO>
A:Cross-references: GB:AE002093; NID:g3132473; PIDN:AAC16262.1; GSPDB:GN00139
C:Genetics:

```

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A:Gene: At2g34720; T29F13.7
A:Map position: 2
A:Introns: 44/3; 76/3; 104/3; 159/3

Query Match          3.8%; Score 8; DB 2; Length 226;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
Db 136 HGILRRRQ 143

RESULT 12
T45935
probable galactose oxidase (EC 1.1.3.9) F5K20.250 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 24-Oct-2000
C:Accession: T45935
R:Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer, K.F
submitted to the Protein Sequence Database, January 2000
A:Reference number: Z23017
A:Accession: T45935
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-545 <MON>
A:Cross-references: EMBL:AL132960
A:Experimental source: cultivar Columbia; BAC clone F5K20
C:Genetics:
A:Map position: 3
A:Note: F5K20.250
C:Superfamily: Arabidopsis thaliana hypothetical protein F5K20.250
C:Keywords: copper; metal binding; oxidoreductase
F:116-168/Cross-link: cysteinyltyrosine (Cys-Tyr) #status predicted
F:168,390,391,483/Binding site: copper (Tyr, Tyr, His, His) #status predicted

Query Match          3.8%; Score 8; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 QILPDGSV 85
Db 172 QILPDGSV 179

RESULT 13
F59092
hypothetical protein pX01-14 - Bacillus anthracis virulence plasmid pX01
C:Species: Bacillus anthracis
C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-May-2000
C:Accession: F59092
R:Oknaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koeh
J. Bacteriol. 181, 6509-6515, 1999
A:Title: Sequence and organization of pX01, the large Bacillus anthracis plasmid harb
A:Reference number: A59091; MUID:99445483
A:Accession: F59092
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-564 <OKI>
A:Cross-references: GB:AF065404; NID:g4894216; PIDN:AAD32318.1; PID:g4894230
A:Experimental source: strain Sterne
C:Genetics:
A:Gene: pX01-14
A:Genome: plasmid
C:Superfamily: Bacillus anthracis virulence plasmid pX01 hypothetical protein pX01-14

Query Match          3.8%; Score 8; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 LYGSEKLT 134
Db 329 LYGSEKLT 336

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RESULT 14
T00367
hypothetical protein KIAA0665 - human
C:Species: Homo sapiens (man)
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 21-Jul-2000
C:Accession: T00367
R:Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.
DNA Res. 5, 169-176, 1998
A:Title: Prediction of the coding sequences of unidentified human genes. X. The complete
A:Reference number: Z14142; MUID:98403880
A:Accession: T00367
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-756 <ISH>
A:Cross-references: EMBL:AB014565; NID:g3327143; PIDN:BAA31640.1; PID:g3327144
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0665

Query Match          3.8%; Score 8; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GPGAAQLA 58
      |||||
Db 26 GPGAAQLA 33

RESULT 15
T42229
probable E1-E2 ATPase (EC 3.6.1.-) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C:Accession: T42229
R:Halleck, M.S.; Blackman, C.F.; Gao, L.; Williamson, P.L.; Schlegel, R.A.
submitted to the EMBL Data Library, June 1997
A:Description: Multiple members of a third subfamily of P-type ATPases identified by gen
A:Reference number: Z22089
A:Accession: T42229
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1020 <HAL>
A:Cross-references: EMBL:AF011336; NID:g2944186; PID:g2944187; PIDN:AAC05245.1
C:Keywords: hydrolase; transmembrane protein

Query Match          3.8%; Score 8; DB 2; Length 1020;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PELYKDLL 208
      |||||
Db 880 PELYKDLL 887

Search completed: October 21, 2002, 16:21:25
Job time : 67 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:15:41 ; Search time 13 Seconds

(without alignments)
628.448 Million cell updates/sec

Title: US-09-817-814-2

Perfect score: 211

Sequence: 1 MAPLAEGVGGFLGGLGQQ.....PRVPDPVRPELYKDLLMYT 211

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	100.0	211	1	FGFK_HUMAN
2	20	9.5	209	1	FGF9_XENLA
3	19	9.0	208	1	FGF9_HUMAN
4	19	9.0	208	1	FGF9_MOUSE
5	19	9.0	208	1	FGF9_RAT
6	16	7.6	207	1	FGFG_HUMAN
7	16	7.6	207	1	FGFG_RAT
8	8	3.8	151	1	Y273_METH
9	8	3.8	157	1	YD58_CAUCR
10	8	3.8	756	1	Y665_HUMAN
11	8	3.8	1047	1	AT9A_HUMAN
12	8	3.8	1047	1	AT9A_MOUSE
13	7	3.3	94	1	THEB_HAEIN
14	7	3.3	120	1	CEPL_CERFI
15	7	3.3	142	1	GLBI_LUMTE
16	7	3.3	155	1	RS11_YEAST
17	7	3.3	232	1	HXA6_MOUSE
18	7	3.3	242	1	GSHV_ARATH
19	7	3.3	246	1	MYPO_HETFR
20	7	3.3	252	1	BPE4_HUMAN
21	7	3.3	262	1	PLCL_CAEEL
22	7	3.3	337	1	AT9B_HUMAN
23	7	3.3	391	1	RRPP_MUMPE
24	7	3.3	391	1	RRPP_MUMPM
25	7	3.3	409	1	CAD1_YEAST
26	7	3.3	413	1	L756_CAEEL
27	7	3.3	415	1	BOFH_BRAOL
28	7	3.3	423	1	DHE3_AERPE
29	7	3.3	424	1	LFY_ARATH
30	7	3.3	426	1	TOLB_CHLMU
31	7	3.3	431	1	TOLB_CHLTR
32	7	3.3	460	1	COAA_BP1F1
33	7	3.3	492	1	VHS_HSV2G

34	7	3.3	511	1	IE63_HSV1E
35	7	3.3	512	1	IE63_HSV1I
36	7	3.3	626	1	TESK_HUMAN
37	7	3.3	627	1	TESK_MOUSE
38	7	3.3	628	1	TESK_RAT
39	7	3.3	695	1	TRFL_HORSE
40	7	3.3	708	1	TRFL_CAMDR
41	7	3.3	709	1	MBA2_ECOLI
42	7	3.3	711	1	TRFL_HUMAN
43	7	3.3	739	1	PSAA_SYNPO
44	7	3.3	863	1	IMBL_SCHP2
45	7	3.3	1095	1	AT9B_MOUSE
46	7	3.3	1128	1	DNBL_EBV
47	7	3.3	1856	1	MGA_HUMAN
48	7	3.3	3390	1	POLG_DEN3
49	7	3.3	3403	1	PKD1_HUMAN
50	6	2.8	31	1	PETL_ODOSI
51	6	2.8	57	1	SMS2_PTIAME
52	6	2.8	68	1	MRSA_BACSP
53	6	2.8	78	1	HOLI_BPPI1
54	6	2.8	107	1	URE2_BACSB
55	6	2.8	114	1	PTI3_STYPL
56	6	2.8	118	1	NLT6_AMBAR
57	6	2.8	118	1	YUSI_BACSU
58	6	2.8	123	1	NEF_HV1B1
59	6	2.8	123	1	NEF_HV1H2
60	6	2.8	123	1	URE2_UREPA
61	6	2.8	123	1	URE2_UREUR
62	6	2.8	124	1	LEG_BACSU
63	6	2.8	129	1	LEG_ELEEL
64	6	2.8	135	1	IF2B_METH
65	6	2.8	141	1	GLB_TUBTU
66	6	2.8	141	1	HBAL_NAJNA
67	6	2.8	143	1	YG32_VZVD
68	6	2.8	143	1	YW84_MYCTU
69	6	2.8	144	1	URE2_YERPE
70	6	2.8	145	1	DFP_STRMU
71	6	2.8	145	1	VG46_BPMU
72	6	2.8	146	1	Y4JN_RHISN
73	6	2.8	149	1	CABO_LOLPE
74	6	2.8	151	1	ARGR_HAEIN
75	6	2.8	152	1	RT16_CAEEL
76	6	2.8	154	1	YK01_AERPE
77	6	2.8	155	1	ARGR_PASMU
78	6	2.8	156	1	ARGR_ECOLI
79	6	2.8	156	1	ARGR_SALTY
80	6	2.8	161	1	VANZ_ENTFC
81	6	2.8	163	1	URE2_YEREN
82	6	2.8	174	1	PUR6_MYCTU
83	6	2.8	178	1	VEGA_MYXXA
84	6	2.8	180	1	NEF_HV2NZ
85	6	2.8	183	1	KADA_THEAC
86	6	2.8	186	1	MAUE_PARDE
87	6	2.8	187	1	FGFA_XENLA
88	6	2.8	188	1	FGF59_MFTJA
89	6	2.8	192	1	FGFB_XENLA
90	6	2.8	194	1	FGFA_CHICK
91	6	2.8	199	1	TBP_PYROC
92	6	2.8	202	1	FGF4_MOUSE
93	6	2.8	205	1	NEF_HV1B8
94	6	2.8	205	1	NEF_HV1S3
95	6	2.8	205	1	NEF_SIVCZ
96	6	2.8	206	1	FGF4_BOVIN
97	6	2.8	206	1	FGF4_HUMAN
98	6	2.8	206	1	NEF_HV112
99	6	2.8	206	1	NEF_HV1B1R
100	6	2.8	206	1	NEF_HV1EL
101	6	2.8	206	1	NEF_HV1LW
102	6	2.8	206	1	NEF_HV1PV
103	6	2.8	207	1	NEF_HV1ND
104	6	2.8	207	1	Y214_MYCGE
105	6	2.8	208	1	FGF6_HUMAN
106	6	2.8	208	1	FGF6_MOUSE

P36295	herpes simp
P10238	herpes simp
Q15569	homo sapien
Q70146	mus musculus
Q63572	rattus norv
Q77811	equus cabal
Q9TUM0	canelus dro
P07112	escherichia
P02788	homo sapien
P17154	synecococc
Q13864	schizosacch
P98195	mus musculus
P03227	epstein-bar
Q43451	homo sapien
P27915	d genome po
P98161	homo sapien
P49524	odontella s
P81879	piaractus m
P43683	bacillus sp
P51727	bacterioph
Q07398	bacillus sp
P28205	steyela plic
Q04004	ambrosia ar
Q32175	bacillus su
P03404	human immun
P04601	human immun
Q56558	ureaplasma
P17273	ureaplasma
P71035	bacillus su
P08520	electrophor
Q27797	methanobact
P18202	tubifex tub
Q9PR19	naja naja (
P09285	varicella-z
P96889	mycobacteri
P52314	yersinia pe
Q54433	streptococc
Q9TIV3	bacterioph
P55514	rhizobium s
P14533	lolligo peal
Q45110	haemophilus
Q10129	caenorhabdi
Q9VAD8	aeropyrum p
P57850	pasteurella
P15282	escherichia
P37170	salmonella
Q06242	enterococcu
P31495	yersinia en
P96880	mycobacteri
P07935	myxococcus
P05860	human immun
Q9H1T1	thermoplasm
P29896	paracoccus
P48805	xenopus lae
Q58954	methanococ
P48806	xenopus lae
P48804	gallus gall
P58177	pyrodictium
P114703	mus musculus
P05855	human immun
P19545	human immun
P17664	chimpanzee
P48803	bos taurus
P08620	homo sapien
P04324	human immun
P03406	human immun
P04604	human immun
Q70627	human immun
P03405	human immun
P18801	human immun
P47456	mycoplasma
P10767	homo sapien
P21658	mus musculus

107	6	2.8	208	1	NEF_HV1S1	P19546	human immun	180	2.8	6	2.8	326	1	TF2B_ARCFU	O28970	archaeoglobul
108	6	2.8	210	1	NEF_HV1A2	P03407	human immun	181	2.8	6	2.8	326	1	Y083_CAUCR	P37895	caulobacte
109	6	2.8	211	1	NEF_HV1O2	P20886	human immun	182	2.8	6	2.8	331	1	APA2_KLULA	P49348	kluyveromy
110	6	2.8	212	1	NEF_HV1Z6	P50404	human immun	183	2.8	6	2.8	331	1	TAL_HUMAN	P17542	homo sapien
111	6	2.8	213	1	URE1_HELMO	P50044	helicobacte	184	2.8	6	2.8	332	1	SIX3_HUMAN	O95343	homo sapien
112	6	2.8	213	1	YKGB_HAEIN	P44577	haemophilus	185	2.8	6	2.8	333	1	SIX3_MOUSE	O62233	mus musculus
113	6	2.8	214	1	NEF_HV1Y2	P35959	human immun	186	2.8	6	2.8	338	1	HXDB_HUMAN	P31277	homo sapien
114	6	2.8	216	1	NEF_HV1JR	P20867	human immun	187	2.8	6	2.8	340	1	YDDR_ECOLI	P77308	escherichia
115	6	2.8	217	1	GTM1_HUMAN	P09488	homo sapien	188	2.8	6	2.8	342	1	RTCA_PPRAB	O5V026	pyrococcus
116	6	2.8	217	1	GTM2_HUMAN	P28161	homo sapien	189	2.8	6	2.8	347	1	DDL_STRPB	O54631	streptococc
117	6	2.8	217	1	GTM3_MOUSE	P19639	mus musculus	190	2.8	6	2.8	349	1	VALL1_PHUV	O06923	pepper huas
118	6	2.8	218	1	LIPB_PASNU	P57977	pasteurella	191	2.8	6	2.8	350	1	R51B_MOUSE	O35719	mus musculus
119	6	2.8	218	1	NEF_HV1BN	P12479	human immun	192	2.8	6	2.8	352	1	VALL1_TGMV	P03567	tomato gold
120	6	2.8	220	1	TPIS_CHLAU	P96744	chloroflexu	193	2.8	6	2.8	353	1	VALL1_BGMV	P05175	bean golden
121	6	2.8	220	1	YD41_MYCLE	P52063	mycobacteri	194	2.8	6	2.8	354	1	MAT1_COCCV	O9Y8D1	cochliobolu
122	6	2.8	221	1	SCRK_SALTH	P24261	salmonella	195	2.8	6	2.8	355	1	VALL1_ARMVW	P21947	abutilon mo
123	6	2.8	223	1	YUG4_CAEL	P91851	caenorhabdi	196	2.8	6	2.8	356	1	CCDA_CAEL	P35800	caenorhabdi
124	6	2.8	228	1	2313_HUMAN	O9Y508	homo sapien	197	2.8	6	2.8	357	1	VALL1_TYLCV	P27259	tomato yell
125	6	2.8	230	1	CLD2_CANFA	O95kmf6	canis famil	198	2.8	6	2.8	358	1	PE22_HUMAN	P43116	homo sapien
126	6	2.8	230	1	CLD2_HUMAN	P57739	homo sapien	199	2.8	6	2.8	358	1	VALL1_BCTV	P14991	beet curiyy
127	6	2.8	230	1	CLD2_MOUSE	O88552	mus musculus	200	2.8	6	2.8	358	1	VALL1_GLVK	P14982	cassava lat
128	6	2.8	231	1	VHEL_CVB	P37988	chrysanthem	201	2.8	6	2.8	358	1	VALL1_GLVN	P14972	cassava lat
129	6	2.8	231	1	YEJ4_YEAST	P40008	saccharomyc	202	2.8	6	2.8	359	1	VALL1_TYLCM	P27260	tomato yell
130	6	2.8	234	1	URE1_HECHE	P42822	helicobacte	203	2.8	6	2.8	359	1	VALL1_TYLCU	P38609	tomato yell
131	6	2.8	236	1	ABME_RABIT	P47855	oryctolagus	204	2.8	6	2.8	360	1	WNT2_HUMAN	P09544	homo sapien
132	6	2.8	236	1	MLPA_MYXXA	P38371	myxococcus	205	2.8	6	2.8	360	1	WNT2_MOUSE	P21552	mus musculus
133	6	2.8	236	1	UBL1_YEAST	P35127	saccharomyc	206	2.8	6	2.8	361	1	VALL1_PMVV	P27258	potato yell
134	6	2.8	237	1	URE1_HELPF	O08715	helicobacte	207	2.8	6	2.8	361	1	VALL1_TMOV	O06657	tomato mott
135	6	2.8	237	1	2198_MOUSE	O9cu65	mus musculus	208	2.8	6	2.8	362	1	VALL1_TYLCA	P36279	tomato yell
136	6	2.8	238	1	IAH1_YEAST	P41734	saccharomyc	209	2.8	6	2.8	365	1	NMPC_ECOLI	P21420	escherichia
137	6	2.8	239	1	CPW1_YEAST	P28319	saccharomyc	210	2.8	6	2.8	365	1	POR1_BPPA2	P07238	bacterioph
138	6	2.8	239	1	NEF_HV1SC	P05857	human immun	211	2.8	6	2.8	367	1	GCST_MYCLE	O32955	mycobacteri
139	6	2.8	242	1	PYRF_HALM1	O9p9m3	halobacteri	212	2.8	6	2.8	367	1	GCST_MYCTU	O10376	mycobacteri
140	6	2.8	242	1	RECO_ECOLI	P15027	escherichia	213	2.8	6	2.8	368	1	AROC_BACSU	P31104	bacillus su
141	6	2.8	242	1	RECQ_SALTY	Q56058	salmonella	214	2.8	6	2.8	369	1	DAPE_CORGL	O59284	corynebacte
142	6	2.8	243	1	YQ27_CAEL	P34677	caenorhabdi	215	2.8	6	2.8	370	1	CYB_EPIAN	O48041	epicrates a
143	6	2.8	244	1	ARC3_CBCP	Q00901	clostridium	216	2.8	6	2.8	370	1	CYB_EPIFO	O48049	epicrates f
144	6	2.8	245	1	T2P7_PSEAE	P05104	pseudomonas	217	2.8	6	2.8	370	1	CYB_EPISU	O48062	epicrates s
145	6	2.8	246	1	AXB_ARATH	P38829	arabidopsis	218	2.8	6	2.8	370	1	CYB_EUNMU	O48063	eunectes mu
146	6	2.8	255	1	NEF_HV2ST	P20868	human immun	219	2.8	6	2.8	370	1	CYB_EUNNO	O48065	eunectes no
147	6	2.8	255	1	UNG_HSV6U	P52345	human herpe	220	2.8	6	2.8	371	1	CYB_ANISC	O48014	anillus scy
148	6	2.8	255	1	UNG_HSV62	P2447	human herpe	221	2.8	6	2.8	371	1	CYB_EPIMO	O48052	epicrates m
149	6	2.8	255	1	Y584_CAEL	Q09381	caenorhabdi	222	2.8	6	2.8	371	1	CYB_ERYEL	O48073	eryx elega
150	6	2.8	260	1	NEF_HV2CA	P24103	human immun	223	2.8	6	2.8	371	1	CYB_ERYJA	O48076	eryx jaculu
151	6	2.8	262	1	BPHF_SPHAR	O86013	sphingomona	224	2.8	6	2.8	371	1	CYB_ERYMI	O48079	eryx miliar
152	6	2.8	264	1	FGF5_MOUSE	P15656	mus musculus	225	2.8	6	2.8	371	1	CYB_ERYMN	O48080	eryx miliar
153	6	2.8	265	1	YCRJ_ECOLI	P76044	escherichia	226	2.8	6	2.8	371	1	CYB_ERYTA	O48085	eryx tatari
154	6	2.8	266	1	FGF5_RAT	P48807	rattus norv	227	2.8	6	2.8	371	1	CYB_LATCO	Q9mJ4	laticauda c
155	6	2.8	268	1	FGF5_HUMAN	P12034	homo sapien	228	2.8	6	2.8	372	1	AGI_URTIC	P11218	urtica dioi
156	6	2.8	273	1	G80_BACSU	Q08078	bacillus su	229	2.8	6	2.8	374	1	RGSK_BOVIN	P79348	bos taurus
157	6	2.8	276	1	D101_ARATH	Q05211	arabidopsis	230	2.8	6	2.8	375	1	YY10_MYCTU	O50716	mycobacteri
158	6	2.8	277	1	TRPC_PSEPU	P20578	pseudomonas	231	2.8	6	2.8	376	1	OMPC_SERMA	O54471	serratia ma
159	6	2.8	288	1	LIVE_METJA	Q36414	methanococc	232	2.8	6	2.8	378	1	RUI7_MOUSE	O62376	mus musculus
160	6	2.8	288	1	PDXK_SALTY	P40192	salmonella	233	2.8	6	2.8	381	1	GRK1_ECOLI	P77364	escherichia
161	6	2.8	295	1	TFDR_ALCEU	P10086	alcaligenes	234	2.8	6	2.8	381	1	RODA_HELPY	P56098	helicobacte
162	6	2.8	296	1	YF23_HAEIN	P44243	haemophilus	235	2.8	6	2.8	383	1	Y987_METTH	O27068	methanobact
163	6	2.8	300	1	CYB_PLAGA	P81376	plasmodium	236	2.8	6	2.8	387	1	CTRA_NEIMA	P32758	neisseria m
164	6	2.8	303	1	NQRF_ALTHA	Q91CJ4	alteromonas	237	2.8	6	2.8	388	1	AROC_STAAU	O59803	staphylococ
165	6	2.8	303	1	NQRF_COLMA	Q9K3E1	colwellia m	238	2.8	6	2.8	389	1	SL7P_CHLRE	P46284	chlamydomon
166	6	2.8	303	1	NQRF_PHOPO	Q91CJ1	photobacter	239	2.8	6	2.8	391	1	CTRA_NEIMB	P32013	neisseria m
167	6	2.8	303	1	NQRF_SHEHA	Q91C18	shewanella	240	2.8	6	2.8	391	1	UVSX_BPT4	P04529	bacterioph
168	6	2.8	303	1	NQRF_VIBMA	Q91C19	vibrio mari	241	2.8	6	2.8	394	1	NQPB_SCHPO	Q10088	schizosacch
169	6	2.8	303	1	NQRF_VIBPA	Q91CJ0	vibrio para	242	2.8	6	2.8	397	1	AXP_YARLI	Q92389	yarrowia li
170	6	2.8	303	1	NQRF_VIBPS	Q91CJ2	vibrio psyc	243	2.8	6	2.8	397	1	YEDS_ECOLI	P76335	escherichia
171	6	2.8	304	1	PTFB_BACAM	P41029	bacillus am	244	2.8	6	2.8	401	1	RL3_CAEL	P50880	caenorhabdi
172	6	2.8	307	1	SCRK_SALTY	P26984	salmonella	245	2.8	6	2.8	403	1	CHEB_TREPA	O83639	treponema p
173	6	2.8	310	1	CNO7_CAEL	Q17345	caenorhabdi	246	2.8	6	2.8	405	1	NQRF_NEIMA	O9JYV3	neisseria m
174	6	2.8	312	1	K1PF_ECOLI	P23539	escherichia	247	2.8	6	2.8	405	1	NQRF_NEIMB	Q9JK08	neisseria m
175	6	2.8	313	1	EBAG_STREL	P04067	streptomyce	248	2.8	6	2.8	407	1	NQRF_PASMU	O9C1A6	pasteurella
176	6	2.8	313	1	K1PF_HAEIN	P44330	haemophilus	249	2.8	6	2.8	407	1	NQRF_VIBAL	O56584	v na(+)-tra
177	6	2.8	316	1	ATPG_SYN56	P08450	synechococc	250	2.8	6	2.8	407	1	NQRF_VIBHA	Q9RFV6	vibrio harv
178	6	2.8	317	1	RCN2_HUMAN	Q14257	homo sapien	251	2.8	6	2.8	408	1	NQRF_VIBCH	O9X4Q8	vibrio chol
179	6	2.8	323	1	HXDB_MOUSE	P23813	mus musculus	252	2.8	6	2.8	409	1	NER1_MOUSE	O35657	mus musculus

253	6	2.8	409	1	NER1_RAT	Q99pw3	rattus norv	326	6	2.8	550	1	THDH_ARXAD	O42615	arxula aden
254	6	2.8	411	1	NORF_HAEIN	O05012	haemophilus	327	6	2.8	556	1	AGM1_ARATH	P57750	arabidopsis
255	6	2.8	413	1	GLYA_BACHD	Q9K694	bacillus su	328	6	2.8	556	1	PHL_LEPIN	P17627	leptospira
256	6	2.8	414	1	QYH_BACSU	P54545	bacillus su	329	6	2.8	557	1	HLVB_SERMA	P15321	serratia ma
257	6	2.8	415	1	NER1_HUMAN	Q99519	homo sapien	330	6	2.8	557	1	MAOX_PIG	Q29558	sus scrofa
258	6	2.8	418	1	EPF2_RALSO	O45412	raistonia s	331	6	2.8	559	1	PHF1_MOUSE	Q921b8	mus musculus
259	6	2.8	419	1	PGK_TREPA	O83549	treponema p	332	6	2.8	562	1	YMX8_YEAST	O04301	saccharomyc
260	6	2.8	419	1	SYS_MYCTU	P96244	mycobacteri	333	6	2.8	567	1	PHF1_HUMAN	O43189	homo sapien
261	6	2.8	426	1	APEB_MYCLE	Q50022	mycobacteri	334	6	2.8	576	1	T2BR_BACSU	P06529	bacillus su
262	6	2.8	426	1	GLAI_MYCTU	O53441	mycobacteri	335	6	2.8	589	1	RLP3_RAT	O88671	rattus norv
263	6	2.8	426	1	GLYA_MYCLE	Q9X794	mycobacteri	336	6	2.8	589	1	RRPO_BQBE	P14647	bacterioph
264	6	2.8	426	1	AROA_BUCAI	P57396	buchnera ap	337	6	2.8	591	1	PAK4_HUMAN	O96013	homo sapien
265	6	2.8	427	1	TRBL_AERPE	Q9Y8T5	aeropyrum p	338	6	2.8	592	1	DLL3_MOUSE	O88516	mus musculus
266	6	2.8	428	1	OM47_PASMU	P80603	pasteurella	339	6	2.8	596	1	NOLX_RHISN	P55711	rhizobium s
267	6	2.8	429	1	AG45_MYCLE	P46838	mycobacteri	340	6	2.8	596	1	Y4IJ_RHISN	P55493	rhizobium s
268	6	2.8	429	1	URAA_ECOLI	P33780	escherichia	341	6	2.8	604	1	YJ16_YEAST	P47112	saccharomyc
269	6	2.8	432	1	PYRP_BACCL	P41006	bacillus ca	342	6	2.8	607	1	PHEA_PSESP	P31020	pseudomonas
270	6	2.8	433	1	APEB_MYCTU	O06634	mycobacteri	343	6	2.8	617	1	MUTA_PORGI	Q59676	porphyromon
271	6	2.8	433	1	ENO_BORBU	O51312	borrelia bu	344	6	2.8	617	1	SYP_SYNY3	P73942	synechocyst
272	6	2.8	434	1	PYRP_BACSU	P39766	bacillus su	345	6	2.8	618	1	T2D5_XENLA	Q91857	xenopus lae
273	6	2.8	437	1	RUI17_HUMAN	P08621	homo sapien	346	6	2.8	620	1	AFR1_YEAST	P33304	saccharomyc
274	6	2.8	439	1	PHT3_PSEPU	Q05183	pseudomonas	347	6	2.8	630	1	SOHC_ALIAC	P33247	alicyclobac
275	6	2.8	439	1	SNDR_ACELI	Q44091	acetobacter	348	6	2.8	636	1	CAI3_RAT	P13941	rattus norv
276	6	2.8	451	1	TBG_ENTHI	P54401	entamoeba h	349	6	2.8	637	1	P73_CERAE	Q9XSK8	cercopithec
277	6	2.8	451	1	MUC_SUNMU	P20768	suncus muri	350	6	2.8	643	1	DNAI_STRRE	Q9Zn76	streptomyce
278	6	2.8	457	1	VSG2_TRYEQ	P20950	trypanosoma	351	6	2.8	655	1	ACDV_HUMAN	P49748	homo sapien
279	6	2.8	460	1	MERA_SERMA	P08662	serratia ma	352	6	2.8	656	1	YC26_PORPU	P51392	porphyra pu
280	6	2.8	462	1	ANFK_AZOVI	P16267	azotobacter	353	6	2.8	661	1	MX1_HUMAN	P20591	homo sapien
281	6	2.8	463	1	YI02_MYCTU	O53951	mycobacteri	354	6	2.8	662	1	IL2R_HUMAN	P42701	homo sapien
282	6	2.8	464	1	AAK1_PIG	Q9MYP4	sus scrofa	355	6	2.8	666	1	YJB0_YEAST	P47077	saccharomyc
283	6	2.8	465	1	EXSH_RHIME	O33680	rhizobium m	356	6	2.8	669	1	YU06_HAEIN	P45335	haemophilus
284	6	2.8	465	1	VP19_HSV11	P32888	herpes simp	357	6	2.8	674	1	NUOL_NEIMA	Q9JX92	neisseria m
285	6	2.8	465	1	VP19_HSV14	P17586	herpes simp	357	6	2.8	674	1	NUOL_NEIMA	Q9K1b0	neisseria m
286	6	2.8	466	1	VP19_HSV2G	P22486	herpes simp	358	6	2.8	674	1	NUOL_NEIMA	Q11780	sus scrofa
287	6	2.8	467	1	CPXR_RHISN	P55543	rhizobium s	359	6	2.8	683	1	BGH3_PIG	Q9RWH3	deinococcus
288	6	2.8	467	1	IRF6_HUMAN	O14896	homo sapien	360	6	2.8	690	1	VATI_DEIRA	P15713	pseudomonas
289	6	2.8	467	1	IRF6_MOUSE	P97431	mus musculus	361	6	2.8	692	1	PHLN_PSERE	P79763	gallus gall
290	6	2.8	473	1	ERIC_EGO57	P58244	escherichia	362	6	2.8	693	1	FSHR_CHICK	Q10801	mycobacteri
291	6	2.8	473	1	ERIC_ECOLI	P37019	escherichia	363	6	2.8	695	1	DIP2_MYCTU	P13989	escherichia
292	6	2.8	476	1	RRG1_XENLA	P51127	xenopus lae	364	6	2.8	702	1	TNSB_ECOLI	P32775	saccharomyc
293	6	2.8	480	1	GAT2_HUMAN	P23769	homo sapien	365	6	2.8	704	1	GLGB_YEAST	Q01992	rattus norv
294	6	2.8	480	1	GAT2_MOUSE	O09100	mus musculus	366	6	2.8	710	1	PMIP_RAT	P21169	escherichia
295	6	2.8	481	1	YFL4_YEAST	P43616	saccharomyc	367	6	2.8	711	1	DCOR_ECOLI	P21169	escherichia
296	6	2.8	483	1	PANF_ECOLI	P16256	escherichia	368	6	2.8	718	1	CTPC_MYCTU	P96875	mycobacteri
297	6	2.8	484	1	KPYK_CHLPN	Q92984	chlamydia p	369	6	2.8	731	1	KCN3_MOUSE	P58391	mus musculus
298	6	2.8	484	1	PANF_HAEIN	P44963	haemophilus	370	6	2.8	732	1	DCOS_ECOLI	P24169	escherichia
299	6	2.8	484	1	PIGA_HUMAN	P37287	homo sapien	371	6	2.8	732	1	KCN3_RAT	P70605	rattus norv
300	6	2.8	486	1	YGI2_AQUAE	P67542	aquifex aeo	372	6	2.8	740	1	GAG_SMRVH	P21411	squirrel mo
301	6	2.8	490	1	C72T_ARATH	Q9Sae4	arabidopsis	373	6	2.8	774	1	STF_LAMBD	P03764	bacterioph
302	6	2.8	491	1	HEMN_ALCEU	O34162	alcaligenes	374	6	2.8	779	1	ACON_GRAVE	P49609	gracilaria
303	6	2.8	496	1	NANT_ECOLI	P41036	escherichia	375	6	2.8	781	1	NANH_VIBCH	P37060	vibrio chol
304	6	2.8	500	1	CPN2_MOUSE	P15539	mus musculus	376	6	2.8	784	1	DPO2_AERPE	Q93746	aeropyrum p
305	6	2.8	501	1	ATPA_ACEWO	P50000	acetobacter	377	6	2.8	796	1	TRKA_HUMAN	P04629	homo sapien
306	6	2.8	501	1	MYSU_RABIT	Q99105	oryctolagus	378	6	2.8	799	1	TRKA_RAT	P35739	rattus norv
307	6	2.8	503	1	VATE_SCHPO	P31411	schizosacch	379	6	2.8	802	1	XPB_DROME	Q02870	drosophila
308	6	2.8	503	1	YS97_MYCTU	Q10818	mycobacteri	380	6	2.8	806	1	SUBV_BACSU	P29141	bacillus su
309	6	2.8	504	1	ATIN_HSVBP	P30020	bovine herp	381	6	2.8	819	1	AK1H_SERMA	P27725	serratia ma
310	6	2.8	504	1	IRF5_HUMAN	Q13568	homo sapien	382	6	2.8	825	1	QUTA_EMENI	P10363	emeritella
311	6	2.8	505	1	SYK1_MYCTU	O06284	mycobacteri	383	6	2.8	830	1	DYNI_CAEEL	P39055	caenorhabd
312	6	2.8	506	1	GUX2_AGABE	Q92400	agarcus bi	384	6	2.8	831	1	NAPA_ALCEU	P39185	alcaligenes
313	6	2.8	512	1	GLPD_PSEAE	P52111	pseudomonas	385	6	2.8	831	1	NAPA_PARDT	Q56350	paracoccus
314	6	2.8	512	1	HUTH_STRCO	Q9eww1	streptomyce	386	6	2.8	833	1	DL_DROME	P10041	drosophila
315	6	2.8	512	1	KAPB_SCHPO	P40376	schizosacch	387	6	2.8	833	1	PTIA_ECOLI	P32670	escherichia
316	6	2.8	513	1	NHAB_ECOLI	P27377	escherichia	388	6	2.8	834	1	MSH5_HUMAN	Q43196	homo sapien
317	6	2.8	514	1	HUTH_STRGR	P24221	streptomyce	389	6	2.8	836	1	GCSI_HUMAN	Q13724	homo sapien
318	6	2.8	514	1	NREA_SULDE	Q924p4	sulfurospir	390	6	2.8	836	1	PDC2_CANAL	O60035	candida alb
319	6	2.8	516	1	Y369_TREPA	O83384	treponema p	391	6	2.8	839	1	PHLD_BOVIN	P80109	bos taurus
320	6	2.8	523	1	MMSA_CAEEL	P52713	caenorhabd	392	6	2.8	854	1	KDPD_RATRA	O34971	rathayibact
321	6	2.8	531	1	NUON_MYCTU	O53308	mycobacteri	393	6	2.8	855	1	NOLI_HUMAN	P46087	homo sapien
322	6	2.8	535	1	CP27_RABIT	P17177	cytochrom	394	6	2.8	863	1	DPP6_BOVIN	P42659	bos taurus
323	6	2.8	541	1	TLC2_CHLTR	O84502	chlamydia t	395	6	2.8	865	1	ALKS_PSEOL	P42658	homo sapien
324	6	2.8	541	1	Y4MM_RHISN	P55572	rhizobium s	396	6	2.8	882	1	NODV_BRAJA	P17051	pseudomonas
325	6	2.8	544	1	MKR3_MOUSE	Q60764	mus musculus	397	6	2.8	889	1	ATX7_HUMAN	P15939	bradyrhizob
								398	6	2.8	892	1		O15265	homo sapien

399	1	ATMA_ECOLI	898	2.8	6	P39168	escherichia	472	6	2.8	4393	1	PGBM_HUMAN	P98160	homo sapien
400	1	ATMA_SALTY	902	2.8	6	P36640	salmonella	473	6	2.8	5217	1	HTSI_COCCA	Q01886	cochliobolu
401	1	DM3A_MOUSE	908	2.8	6	O88508	mus musculus	474	6	2.8	32	1	YTK3_ILTVT	P23985	infectious
402	1	DP01_BORBU	908	2.8	6	O51498	borrelia bu	475	5	2.4	33	1	YC12_CHLRE	P50370	chlamydomon
403	1	DM3A_HUMAN	912	2.8	6	O9y6k1	homo sapien	476	5	2.4	44	1	YC9X_ODOSI	P49835	odontella s
404	1	DNL3_HUMAN	922	2.8	6	P49916	homo sapien	477	5	2.4	45	1	GLB2_GLYDI	P02217	glycera dib
405	1	VGLB_HSVBC	932	2.8	6	P12640	bovine herp	478	5	2.4	49	1	R332_TREPA	Q06798	bacillus su
406	1	PAC4_RAT	937	2.8	6	Q63415	rattus norv	479	5	2.4	51	1	RL34_TREPA	O83917	treponema p
407	1	LBPA_NEIMB	943	2.8	6	Q06379	neisseria m	480	5	2.4	56	1	UCRY_BOVIN	P07552	bos taurus
408	1	LBPA_NEIMA	944	2.8	6	O9jtk4	neisseria m	481	5	2.4	56	1	UCRY_HUMAN	O14957	homo sapien
409	1	IF41_YEAST	952	2.8	6	P39935	saccharomyc	482	5	2.4	62	1	YM32_MARPO	P38474	marchantia
410	1	YC07_YEAST	953	2.8	6	P25618	saccharomyc	483	5	2.4	63	1	RL44_AERPE	O9y600	aeropyrum p
411	1	LONM_CAEEL	971	2.8	6	O44952	caenorhabdi	484	5	2.4	64	1	PHYB_PHYBI	P81565	phyllomedus
412	1	RPN1_YEAST	993	2.8	6	P38764	saccharomyc	485	5	2.4	64	1	Y05K_BPT4	P39238	bacterioph
413	1	GLNE_MYCTU	994	2.8	6	Q10379	mycobacteri	486	5	2.4	65	1	YJET_ECOLI	P39289	escherichia
414	1	EPAB_MOUSE	1004	2.8	6	O09127	mus musculus	487	5	2.4	66	1	RLXN_RANCA	P39084	rana catesb
415	1	EPAB_HUMAN	1005	2.8	6	P29322	homo sapien	488	5	2.4	67	1	SAS2_BACSU	P04832	bacillus su
416	1	CA13_BOVIN	1049	2.8	6	P04258	bos taurus	489	5	2.4	67	1	TATE_SALTY	P57050	salmonella
417	1	UBA1_WHEAT	1051	2.8	6	P20973	trititum ae	490	5	2.4	68	1	V07K_PMW	P20954	papaya mosa
418	1	UBA2_WHEAT	1051	2.8	6	P31251	trititum ae	491	5	2.4	69	1	SAS1_BACSU	P04831	bacillus su
419	1	GCSP_PEA	1057	2.8	6	P26969	pisum sativ	492	5	2.4	69	1	Y4LI_RHISN	P55349	rhizobium s
420	1	NUP1_YEAST	1076	2.8	6	P20676	saccharomyc	493	5	2.4	69	1	Y842_ARCFU	O29416	archaeoglob
421	1	T2D3_HUMAN	1083	2.8	6	O00268	homo sapien	494	5	2.4	70	1	KAD_STRSC	P43417	streptomyc
422	1	IMB3_YEAST	1089	2.8	6	P32337	saccharomyc	495	5	2.4	70	1	MTRF_METMA	P80654	methanosarc
423	1	KPCI_ASPNG	1096	2.8	6	Q00078	aspergillus	496	5	2.4	70	1	SAS1_BACST	P06552	bacillus sc
424	1	MYSB_ACACA	1131	2.8	6	P08004	saccharomyc	497	5	2.4	70	1	YAI2_ECOLI	P77273	escherichia
425	1	CHS4_WAGGR	1147	2.8	6	P19706	acanthamoeb	498	5	2.4	72	1	UCRX_SOLTU	P46270	solanum tub
426	1	XMRK_XIPMA	1167	2.8	6	P13388	xiphophorus	499	5	2.4	74	1	IRX1_MOUSE	P81068	mus musculus
427	1	SRS2_YEAST	1175	2.8	6	P12954	saccharomyc	500	5	2.4	74	1	YIDD_LEPIN	O50638	leptospira
428	1	PIB2_HUMAN	1181	2.8	6	Q00722	homo sapien	501	5	2.4	76	1	GTH_BRAOL	P48438	brassica ol
429	1	CHS4_WAGGR	1198	2.8	6	O13353	magnaporthe	502	5	2.4	78	1	PHI0_HOLTU	P14309	holothuria
430	1	CA13_CHICK	1262	2.8	6	P12105	gallus gall	503	5	2.4	78	1	YO09_BPL2	P42544	bacterioph
431	1	NGCA_CHICK	1266	2.8	6	Q03696	gallus gall	504	5	2.4	81	1	NNAT_HUMAN	Q16517	homo sapien
432	1	DYNA_NEUCR	1300	2.8	6	Q01397	neurospora	505	5	2.4	81	1	NNAT_MOUSE	O61979	mus musculus
433	1	YMD9_YEAST	1328	2.8	6	Q03434	saccharomyc	506	5	2.4	81	1	NNAT_RAT	O62649	rattus norv
434	1	YME4_YEAST	1328	2.8	6	Q04711	saccharomyc	507	5	2.4	82	1	YVCC_VACCC	P21121	vaccinia vi
435	1	YMT5_YEAST	1328	2.8	6	Q04214	saccharomyc	508	5	2.4	87	1	VPR_HV2BE	P18100	human immu
436	1	YMO0_YEAST	1328	2.8	6	Q04670	saccharomyc	509	5	2.4	88	1	RL27_MYCLE	Q9c523	mycobacteri
437	1	CA21_ONCMY	1356	2.8	6	O93484	oncorhynch	510	5	2.4	89	1	COXJ_DROME	Q9vhs2	drosophila
438	1	Z198_HUMAN	1377	2.8	6	Q9ubw7	homo sapien	511	5	2.4	89	1	DRPH_ROMMI	P09929	romalea mic
439	1	RROP_P1AMV	1385	2.8	6	Q007518	plantago as	512	5	2.4	89	1	RPOK_AERPE	O9yjd19	aeropyrum p
440	1	GTFD_STRMU	1462	2.8	6	P49331	streptococc	513	5	2.4	90	1	AF1Q_HUMAN	Q13015	homo sapien
441	1	CA13_HUMAN	1466	2.8	6	O70167	mus musculus	514	5	2.4	90	1	AF1Q_MOUSE	P97783	mus musculus
442	1	PK3G_MOUSE	1506	2.8	6	P02461	homo sapien	515	5	2.4	90	1	DBH1_BACHD	Q9kda5	bacillus ha
443	1	YJ29_YEAST	1755	2.8	6	P47098	saccharomyc	516	5	2.4	90	1	DBHE_SERMA	P52681	serratia ma
444	1	YJ29_YEAST	1755	2.8	6	P47100	saccharomyc	517	5	2.4	90	1	REV_HV1ZH	P05868	human immu
445	1	MOT1_YEAST	1867	2.8	6	P32333	saccharomyc	518	5	2.4	92	1	DBH1_BACSU	P08821	bacillus su
446	1	PTPF_HUMAN	1897	2.8	6	P10586	homo sapien	519	5	2.4	92	1	IAPP_MESAU	P23442	mesocricetu
447	1	PTPD_HUMAN	1912	2.8	6	P23468	homo sapien	520	5	2.4	92	1	PR10_GAVPO	P20658	cavia porce
448	1	MYHA_BOVIN	1976	2.8	6	Q27991	bos taurus	521	5	2.4	93	1	LI0K_RAT	Q05310	rattus norv
449	1	MYHA_HUMAN	1976	2.8	6	P35580	homo sapien	522	5	2.4	93	1	N36B_SOYBN	Q02919	glycine max
450	1	MYHA_RAT	1976	2.8	6	Q9j1t0	rattus norv	523	5	2.4	93	1	Y073_METJA	O60379	methanococc
451	1	CIN5_RAT	2019	2.8	6	P15389	rattus norv	524	5	2.4	94	1	AFP_ASPGI	P17737	aspergillus
452	1	FSH_DROME	2038	2.8	6	P13709	drosophila	525	5	2.4	94	1	DEF5_HUMAN	Q01523	homo sapien
453	1	TEGU_HSV7J	2059	2.8	6	P52362	human herpe	526	5	2.4	95	1	DAFT_TRYCR	Q26327	trypanosoma
454	1	RRPL_VSVJH	2109	2.8	6	P13615	vesicular s	527	5	2.4	95	1	NQOB_THETH	Q56226	thermus aqu
455	1	RRPL_VSVJO	2109	2.8	6	P16379	vesicular s	528	5	2.4	95	1	YBUC_ECOLI	P46119	escherichia
456	1	RRPL_VSVSJ	2109	2.8	6	P03523	vesicular s	529	5	2.4	95	1	YF03_CLOPE	Q46213	clostridium
457	1	RRPL_RABVS	2127	2.8	6	P16289	rabies viru	530	5	2.4	96	1	CTC1_ACILW	O33947	acinetobact
458	1	RRPL_RABVP	2142	2.8	6	P11213	rabies viru	531	5	2.4	96	1	APC3_MOUSE	P33622	mus musculus
459	1	CCAE_RABIT	2259	2.8	6	Q02343	oryctolagus	532	5	2.4	99	1	PLAS_CUCSA	P00293	cucumis sat
460	1	POUG_EMCV	2290	2.8	6	P03304	encephalomy	533	5	2.4	99	1	PYY_DICUA	O9pt99	dicentrarch
461	1	POUG_EMCVB	2292	2.8	6	P17593	encephalomy	534	5	2.4	99	1	YIAB_YEAST	P40594	saccharomyc
462	1	POUG_EMCVD	2292	2.8	6	P17594	encephalomy	535	5	2.4	99	1	YY07_MYCTU	Q50718	mycobacteri
463	1	FAS_HUMAN	2304	2.8	6	P49327	homo sapien	536	5	2.4	100	1	CXGK_CONGE	P07231	conus geogr
464	1	POIG_BCMVN	3066	2.8	6	Q65399	b genome po	537	5	2.4	100	1	PINL_HUMAN	O15428	homo sapien
465	1	ERY3_SACER	3172	2.8	6	Q03133	saccharopol	538	5	2.4	100	1	YE94_MYCTU	P71775	mycobacteri
466	1	POUG_DEN4	3366	2.8	6	P09866	d genome po	539	5	2.4	100	1	YOG4_CAEEL	P34613	caenorhabdi
467	1	POUG_LANVT	3414	2.8	6	P29837	l genome po	540	5	2.4	101	1	APC2_CANFA	P12278	canis famil
468	1	ERY2_SACER	3567	2.8	6	Q03132	saccharopol	541	5	2.4	101	1	CH10_HUMAN	Q04984	homo sapien
469	1	YAMB_SCHPO	3655	2.8	6	Q10064	schizosacch	542	5	2.4	101	1	CH10_MOUSE	Q64433	mus musculus
470	1	PGBM_MOUSE	3707	2.8	6	Q05793	mus musculus	543	5	2.4	101	1	CH10_RAT	P26772	rattus norv
471	1	PRKD_HUMAN	4128	2.8	6	P78527	homo sapien	544	5	2.4	101	1	ELAB_ECOLI	P52084	escherichia

545	5	2.4	101	1	RS10_BACSU	P21471	618	5	2.4	112	1	GLNB_ECOLI	P05826	escherichia
546	5	2.4	101	1	RS10_BRAPL	Q9fa05	619	5	2.4	112	1	GLNB_KLEFI	P11671	klebsiella
547	5	2.4	101	1	RS10_TREHY	P52857	620	5	2.4	112	1	OSME_ECOLI	P23933	escherichia
548	5	2.4	101	1	RS10_UREPA	P5p101	621	5	2.4	112	1	RLA4_CLAHE	P42039	cladosporiu
549	5	2.4	101	1	SAF_STRGR	Q95109	622	5	2.4	112	1	SV27_HUMAN	Q9y4x3	homo sapien
550	5	2.4	101	1	URE2_ACTPL	O54419	623	5	2.4	112	1	Y112_ADE02	P03289	human adeno
551	5	2.4	101	1	URE2_RHAIN	P44392	624	5	2.4	113	1	RLA2_ALCPAL	P42037	alternaria
552	5	2.4	101	1	URE2_RHIME	P42886	625	5	2.4	113	1	YAC7_ALFAL	P27749	alcaligenes
553	5	2.4	102	1	RS10_BACHD	Q9z915	626	5	2.4	113	1	YFES_CLOPA	Q04624	clostridium
554	5	2.4	102	1	RS10_CAUCR	Q9a8v4	627	5	2.4	114	1	GTH1_FUNHE	P30971	fungulus he
555	5	2.4	102	1	RS10_CLOAB	Q97eh7	628	5	2.4	114	1	VPD6_SCHPO	O14450	schizosacch
556	5	2.4	102	1	RS10_LACLA	Q9cdw1	629	5	2.4	115	1	VPW_BBP2	P51768	bacterioph
557	5	2.4	102	1	RS10_LEPIN	Q9xd37	630	5	2.4	115	1	Y128_TREPA	O83165	treponema p
558	5	2.4	102	1	RS10_MYCCA	P10129	631	5	2.4	115	1	YF36_BAEIN	P44247	haemophilus
559	5	2.4	102	1	RS10_RHIL0	Q98n58	632	5	2.4	116	1	AQN3_PIG	P24020	su. scrofa
560	5	2.4	102	1	RS10_STRMU	P48853	633	5	2.4	116	1	RT10_RECAM	O21246	reclinomona
561	5	2.4	102	1	RS10_STRPN	Q97sv6	634	5	2.4	116	1	Y998_RHIME	Q52966	rhizobium m
562	5	2.4	102	1	RS10_STRPY	Q9aix5	635	5	2.4	116	1	Y75076_MYCPL	P75076	mycoplasma
563	5	2.4	102	1	RS10_TREPA	O83218	636	5	2.4	117	1	HIA1_DICDI	P13231	dictyosteli
564	5	2.4	102	1	RT10_MARPO	P26869	637	5	2.4	117	1	HIA2_DICDI	P42526	dictyosteli
565	5	2.4	102	1	URE2_BORBR	O06707	638	5	2.4	117	1	NLTP_BETVU	Q43748	beta vulgar
566	5	2.4	102	1	URE2_CLOPE	P94668	639	5	2.4	117	1	Y1MJO_CAEEL	P34485	caenorhabdi
567	5	2.4	102	1	VAM5_MOUSE	Q9z2p8	640	5	2.4	118	1	HML2_HIRME	P21523	hirudo medi
568	5	2.4	102	1	YO26_BPHP1	P51730	641	5	2.4	118	1	YRJ5_CAEEL	Q09411	caenorhabdi
569	5	2.4	103	1	RS10_BORBU	P94266	642	5	2.4	119	1	Y618_TREPA	O83627	treponema p
570	5	2.4	103	1	RS10_CAMJE	Q9plx0	643	5	2.4	120	1	MERD_SHIFL	P20102	shigella fl
571	5	2.4	103	1	RS10_MYCPU	Q98px9	644	5	2.4	120	1	ML1B_RAT	P49287	rattus norv
572	5	2.4	103	1	URE2_STRSL	Q55054	645	5	2.4	120	1	VG19_BPMU	Q38646	bacterioph
573	5	2.4	104	1	CHI0_SCHPO	O59804	646	5	2.4	120	1	Y069_ARCFU	Q30167	archaeoglob
574	5	2.4	104	1	RK21_PORPU	P51209	647	5	2.4	121	1	GLN2_METMP	P71525	metnoco
575	5	2.4	104	1	RK25_PEA	P11892	648	5	2.4	121	1	MERD_PSEAE	P06689	pseudomonas
576	5	2.4	104	1	RL3E_SULAC	P11522	649	5	2.4	121	1	MERD_SERMA	P08654	serratia ma
577	5	2.4	104	1	RNC2_ASPLC	P00652	650	5	2.4	121	1	RS10_MYCGA	O52331	mycoplasma
578	5	2.4	104	1	RS10_HELPY	P56017	651	5	2.4	121	1	VOR4_P1AMV	Q07520	plantago as
579	5	2.4	104	1	URE2_MYCTU	P50048	652	5	2.4	121	1	Y378_AQUAE	O67787	aquifex aeo
580	5	2.4	105	1	FER3_RHISN	P55678	653	5	2.4	122	1	HKK_EMENI	P00581	emeritcella
581	5	2.4	105	1	INS_BOVIN	P01317	654	5	2.4	122	1	INL3_MOUSE	O09107	mus musculus
582	5	2.4	105	1	INS_SHEEP	P01318	655	5	2.4	122	1	TERB_ALCSP	P18779	alcaligenes
583	5	2.4	105	1	RS10_CHLPN	Q92803	656	5	2.4	122	1	UROC_MOUSE	P81615	mus musculus
584	5	2.4	105	1	RS10_CHLTR	O84443	657	5	2.4	122	1	UROC_RAT	P55090	rattus norv
585	5	2.4	105	1	RS10_RICPR	P48850	658	5	2.4	123	1	ABA4_TRIAB	P81114	trimeresuru
586	5	2.4	105	1	TH11_SYNY3	P52232	659	5	2.4	123	1	RLI4_BUCAK	P46176	buchnera ap
587	5	2.4	105	1	URE2_SYNY3	P74386	660	5	2.4	123	1	RLI4_ECOLI	P02411	escherichia
588	5	2.4	105	1	VPR_HV2D1	P17761	661	5	2.4	123	1	RLI4_HAEIN	P44352	haemophilus
589	5	2.4	105	1	CH10_YEAST	P18046	662	5	2.4	124	1	MPP5_HUMAN	Q99546	homo sapien
590	5	2.4	106	1	RS10_MYGE	P38910	663	5	2.4	124	1	NTE2_NEUCR	P87102	neurospora
591	5	2.4	106	1	RS10_MYGHY	P73936	664	5	2.4	124	1	OMPX_CHLTR	O84573	chlamydia t
592	5	2.4	106	1	URE2_KLEAE	O50185	665	5	2.4	124	1	RNPA_CAVPO	P00678	cavia porce
593	5	2.4	106	1	URE2_KLEAE	P18315	666	5	2.4	124	1	UR2_HUMAN	O95399	homo sapien
594	5	2.4	108	1	CPA3_CANPG	P81577	667	5	2.4	124	1	UROC_HUMAN	P55089	homo sapien
595	5	2.4	108	1	RS10_MYCPN	P75581	668	5	2.4	124	1	YB15_HALNI	Q9hgk7	halobacteri
596	5	2.4	108	1	URE2_PROVU	P16123	669	5	2.4	124	1	YG3E_YEAST	P53282	saccharomyc
597	5	2.4	108	1	Y11K_PASVK	Q00336	670	5	2.4	125	1	PFDB_HALNI	Q9hsh0	halobacteri
598	5	2.4	108	1	YDBL_ECOLI	P76076	671	5	2.4	125	1	RL7_RICPR	Q9ze21	rickettsia
599	5	2.4	109	1	COXE_RABIT	Q9ttt7	672	5	2.4	125	1	RS11_AQUAE	O66485	aquifex aeo
600	5	2.4	109	1	SEC_HUMAN	P17257	673	5	2.4	125	1	RS6_HAEIN	P44375	haemophilus
601	5	2.4	109	1	URE2_PROMI	P17087	674	5	2.4	125	1	YM88_MYCTU	Q50677	mycobacteri
602	5	2.4	110	1	INS2_MOUSE	P01326	675	5	2.4	126	1	BLAI_STAAR	P18415	staphylococ
603	5	2.4	110	1	INS2_RAT	P01323	676	5	2.4	126	1	PAND_CAMJE	Q9p1k3	campylobact
604	5	2.4	110	1	INS_CERAE	P30407	677	5	2.4	126	1	SYN2_MOUSE	Q64332	mus musculus
605	5	2.4	110	1	INS_CRIL0	P01313	678	5	2.4	126	1	URE2_BACPA	P41021	bacillus pa
606	5	2.4	110	1	INS_HUMAN	P01308	679	5	2.4	126	1	US05_HCMVA	P16840	human cytom
607	5	2.4	110	1	INS_MACFA	P30406	680	5	2.4	127	1	ALL1_SINAL	P15322	sinapis alb
608	5	2.4	110	1	INS_PANTR	P30410	681	5	2.4	127	1	RCRB_CAUCR	Q9afv2	caulobacter
609	5	2.4	110	1	INS_RABIT	P01311	682	5	2.4	127	1	RPB6_HUMAN	P41584	homo sapien
610	5	2.4	110	1	RT10_PEA	P51428	683	5	2.4	127	1	RPB6_RAT	O88828	rattus norv
611	5	2.4	110	1	UVRA_PARDE	P29927	684	5	2.4	128	1	LRP_ORYSA	Q03208	oryza sativ
612	5	2.4	110	1	Y507_METHD	O26607	685	5	2.4	128	1	LRP_ORYSA	Q03200	oryza sativ
613	5	2.4	111	1	COXE_MOUSE	P43024	686	5	2.4	129	1	NUOA_MYCTU	P95181	mycobacteri
614	5	2.4	111	1	COXE_RAT	P10818	687	5	2.4	129	1	ALL1_BRAJU	P80207	brassica ju
615	5	2.4	111	1	OL10_MOUSE	Q60883	688	5	2.4	129	1	PARB_TRYBB	P05791	trypanosoma
616	5	2.4	112	1	CORT_RAT	Q62949	689	5	2.4	130	1	CDD_MYCGE	P47298	mycoplasma
617	5	2.4	112	1	CPA4_CANPG	P81578	690	5	2.4	130	1	ITRY_SINAR	P38057	sinapis arv

691	5	2.4	130	1	MIA_BOVIN	Q28038	bos taurus	764	141	1	DTD_STRCO	Q9k4f6	streptomyc
692	5	2.4	130	1	MIA_MOUSE	O61865	mus musculus	765	141	1	GLBI_PHESE	P11740	pheretima s
693	5	2.4	130	1	MIA_RAT	O62946	rattus norv	766	141	1	HBA_PSIKR	P19831	psittacula s
694	5	2.4	130	1	OREX_CANFA	Q991f6	canis fami	767	141	1	HBA_SPHPU	P10059	sphenodon p
695	5	2.4	130	1	OREX_MOUSE	O55241	mus musculus	768	141	1	PHCO_BPT4	P04538	bacterioph
696	5	2.4	130	1	OREX_RAT	O55232	rattus norv	769	141	1	YC59_LISIN	Q928a6	listeria in
697	5	2.4	130	1	RS11_THEME	Q9x1i4	thermotoga	770	142	1	CDD_YEAST	Q06549	saccharomyc
698	5	2.4	130	1	Y77_BPT7	P03796	bacterioph	771	142	1	CDD_MUSVI	P11280	m corticotr
699	5	2.4	130	1	YE65_AQUAE	O67445	aquifex ao	772	142	1	E1BS_ADE04	P36595	schizosacch
700	5	2.4	130	1	YG31_PYRHO	O59297	pyrococcus	773	142	1	RPB6_SCHPO	P10406	human adeno
701	5	2.4	131	1	AGSR_MOUSE	P56473	mus musculus	774	143	1	RR8_ASTLO	P24353	astasia lon
702	5	2.4	131	1	AGSM_MOUSE	Q03288	mus musculus	775	143	1	BUDR_ENTAE	P52665	enterobacte
703	5	2.4	131	1	AGSM_YULVU	P79407	vulpes vulp	776	143	1	MUCR_RHISN	P11523	sulfolobus
704	5	2.4	131	1	C79A_LOCMI	P45586	locusta mig	777	143	1	NUSA_SULAC	P18663	glycine max
705	5	2.4	131	1	C79B_LOCMI	P45587	locusta mig	778	143	1	RK2_SOYBN	P33118	corynebacte
706	5	2.4	131	1	C007_LOCMI	P11733	locusta mig	779	143	1	YD1L_CORDI	O69561	mycobacteri
707	5	2.4	131	1	MIA_HUMAN	Q16674	homo sapien	780	143	1	YL66_MYCTU	O06211	mycobacteri
708	5	2.4	131	1	OREX_HUMAN	O43612	homo sapien	781	144	1	AGH_ARMVU	Q9u8r2	armadillidi
709	5	2.4	131	1	OREX_PIG	O77668	sus scrofa	782	144	1	GLB3_LAMSP	P15469	lamellibrac
710	5	2.4	131	1	PRO1_SOYBN	O65809	glycine max	783	144	1	GLB3_RIFPA	P80592	riftia pach
711	5	2.4	131	1	PRO2_HALDO	O9xf41	malus domes	784	144	1	GLBB_RIFPA	Q22054	caenorhabdi
712	5	2.4	131	1	PRO2_SOYBN	O65810	glycine max	785	144	1	RS16_CABEL	P14131	mus musculus
713	5	2.4	131	1	PROF_ARAHY	Q98q19	arachis hyp	786	144	1	RS16_MOUSE	O83645	treponema p
714	5	2.4	131	1	RS26_ARATH	P45206	arabidopsis	787	144	1	Y638_TREPA	P56629	aspergillus
715	5	2.4	131	1	RS9_HALMA	P05763	haloarcula	788	145	1	CYB_ASPLI	P56630	aspergillus
716	5	2.4	131	1	RS9_HALN1	Q9hqj2	halobacteri	789	145	1	CYB_ASPLI	P35076	bordetella
717	5	2.4	131	1	V092_POMPV	Q9j5c8	foxiopox vir	790	145	1	FIMA_BORPE	Q38662	bacterioph
718	5	2.4	131	1	Y405_METJA	O57848	methanococc	791	145	1	NINB_BPP22	P17008	homo sapien
719	5	2.4	132	1	AGSR_HUMAN	C00253	homo sapien	792	145	1	RS16_HUMAN	P55686	rhizobium s
720	5	2.4	132	1	AGSM_HUMAN	P41217	homo sapien	793	146	1	Y4WH_RHISN	P41332	microcephal
721	5	2.4	132	1	C560_CYACA	P48935	cyanidium c	794	146	1	NINB_BP221	Q9xj11	bacterioph
722	5	2.4	132	1	CHA2_BOMMO	P08825	bombyx mori	795	146	1	NINB_LAMBD	P03759	bacillus su
723	5	2.4	132	1	SZ05_MOUSE	P50228	mus musculus	796	146	1	YAAR_BACSU	P37539	oncorhynch
724	5	2.4	132	1	YBL2_STRCI	P33654	streptomyc	797	147	1	HBB4_ONCMY	P02140	carassius a
725	5	2.4	132	1	YOHU_ECOLI	P33372	escherichia	798	147	1	HBB_CARAU	P02139	cypripus ca
726	5	2.4	133	1	AGSW_BOVIN	Q29414	bos taurus	799	147	1	HBB_CYPCA	Q98t50	oncorhynch
727	5	2.4	133	1	BRX2_SHEEP	P47718	mycoplasma	800	147	1	HBB_SALSA	Q91473	salmo salar
728	5	2.4	133	1	CDD_MYCPI	P75051	mycoplasma	801	147	1	WZB_ECOLI	P77153	escherichia
729	5	2.4	133	1	CDD_MPCPN	Q01567	erwinia chr	802	147	1	CYTC_RABIT	Q97862	oryctolagus
730	5	2.4	133	1	OUTS_ERWCH	P13976	escherichia	803	148	1	NPIC2_DROME	Q9vq62	tritricum ae
731	5	2.4	133	1	PENK_ECOLI	Q09527	caenorhabdi	804	148	1	PUIB_WHEAT	P43972	haemophilus
732	5	2.4	133	1	YQNC_CABEL	O35216	mus musculus	805	148	1	Y246_HAEIN	Q54235	streptomyc
733	5	2.4	134	1	CENA_MOUSE	P44416	haemophilus	806	148	1	DTD_STRGR	P02220	tylorthynch
734	5	2.4	134	1	OAPB_HAEIN	P15839	oryza sativ	807	149	1	GLB4_TYDHE	P11335	spiroplasma
735	5	2.4	134	1	PRO1_ORYSA	Q9xf37	apium grave	808	149	1	VG3_SPV4	P21863	pseudomonas
736	5	2.4	134	1	PROF_APIGR	P02433	homo sapien	809	149	1	FKBX_PSEPL	Q51467	pseudomonas
737	5	2.4	134	1	RL3P_HUMAN	P17932	mus musculus	810	150	1	FLIO_PSEAE	P14015	brugia paha
738	5	2.4	134	1	RR9_GUITH	P19459	guillardia	811	150	1	RS13_BRUPA	Q9z729	chlamydia p
739	5	2.4	134	1	YHFA_ECOLI	P24246	escherichia	812	150	1	Y877_CHLPH	Q03579	saccharomyc
740	5	2.4	134	1	YHFA_ECOLI	Q33629	apus apus (813	150	1	YMBW_YEAST	P15596	agrobacteri
741	5	2.4	135	1	CYB_APUPA	P30367	bos taurus	814	150	1	DKSA_ECOLI	P18274	escherichia
742	5	2.4	135	1	IL4_BOVIN	P79155	capra hircu	815	151	1	MUP8_MOUSE	Q04938	mus musculus
743	5	2.4	135	1	IL4_CAPHI	P30368	ovis aries	816	151	1	RL19_PYRAB	P091V3	pyrococcus
744	5	2.4	135	1	IL4_SHEEP	P44239	haemophilus	817	151	1	EGFI_PIG	P20002	sus scrofa
745	5	2.4	135	1	VG46_HAEIN	Q17684	caenorhabdi	818	152	1	GLBP_CHIYH	P11582	chironomus
746	5	2.4	135	1	RPB6_CABEL	Q28920	sus scrofa	819	152	1	MYG_APTFO	P79013	schizosacch
747	5	2.4	137	1	SPMI_PIG	P42874	staphylococ	820	152	1	RS11_SCHPO	Q9zcc2	rickettsia
748	5	2.4	137	1	URE2_STAXY	P05462	bacterioph	821	152	1	SSB_RICPR	P32276	bacterioph
749	5	2.4	137	1	ESMA_DROME	Q97178	drosophila	822	152	1	VEL_FPVFL	P06455	avian papil
750	5	2.4	138	1	RS11_MYCLE	Q9x7a0	mycobacteri	823	152	1	Y12G_BPT4	P32761	pseudomonas
751	5	2.4	138	1	VLL_BPV6	P50807	bovine papi	824	153	1	ATP6_PSEPU	P30353	equus cabal
752	5	2.4	138	1	Y087_HUMAN	Q14695	homo sapien	825	153	1	FLAP_HORSE	P02151	aotus crivi
753	5	2.4	138	1	Y560_METJA	O57980	methanococc	826	153	1	MYG_AOTTR	P02179	balaenopter
754	5	2.4	139	1	RS11_MYCBO	P45812	mycobacteri	827	153	1	MYG_BALCP	P02180	balaenopter
755	5	2.4	139	1	RS11_MYCTU	O06326	mycobacteri	828	153	1	MYG_BOVIN	P02152	callithrix
756	5	2.4	139	1	Z014_XENIA	P18740	xenopus lae	829	153	1	MYG_CALJA	P02158	canis fami
757	5	2.4	139	1	CWPX_ARATH	P47925	arabidopsis	830	153	1	MYG_CANFA	P14396	canor fibre
758	5	2.4	140	1	CYB_ASPTPE	P56631	aspergillus	831	153	1	MYG_CBBAP	P02153	cebus apell
759	5	2.4	140	1	RL14_AERPE	Q9yf82	aeropyrum p	832	153	1			
760	5	2.4	140	1	Y236_MYCGE	P47478	mycoplasma	833	153	1			
761	5	2.4	140	1	Y666_MYCPN	P75317	mycoplasma	834	153	1			
762	5	2.4	140	1	YRN3_VIBPA	P46231	vibrio para	835	153	1			
763	5	2.4	140	1				836	153	1			

837	1	MYG_CEREL	153	2.4	5	910	157	1	PRTC_HORSE	Q28380	equus cabal
838	1	MYG_CHICK	153	2.4	5	911	157	1	RS11_DUNTE	P42756	dunaliella
839	1	MYG_CTREGU	153	2.4	5	912	157	1	UL51_HCMVA	P16792	human cytom
840	1	MYG_DIDNA	153	2.4	5	913	158	1	COAD_PASMU	Q9cld4	pasteurella
841	1	MYG_ELEMA	153	2.4	5	914	158	1	LUXS_LACIA	Q9ciu0	lactococcus
842	1	MYG_ERIEU	153	2.4	5	915	158	1	RS11_HUMAN	P04643	homo sapien
843	1	MYG_ESGGI	153	2.4	5	916	158	1	RS11_XENLA	P41115	homo sapien
844	1	MYG_GALCR	153	2.4	5	917	158	1	Y063_UREPA	Q9pr82	ureaplasma
845	1	MYG_GLOME	153	2.4	5	918	158	1	YV02_HUMAN	Q99765	homo sapien
846	1	MYG_GORBE	153	2.4	5	919	159	1	BFR_MYCAV	P43314	mycobacteri
847	1	MYG_HALGR	153	2.4	5	920	159	1	BFR_MYCLE	P43315	mycobacteri
848	1	MYG_HORSE	153	2.4	5	921	159	1	BFR_MYCTU	O08465	mycobacteri
849	1	MYG_HUMAN	153	2.4	5	922	159	1	COAD_ECOLI	P38775	eschericchia
850	1	MYG_HYLAR	153	2.4	5	923	159	1	FABZ_HELPJ	Q9zjl6	helicobacte
851	1	MYG_INLAG	153	2.4	5	924	159	1	FABZ_HELPY	O25928	helicobacte
852	1	MYG_KOGSI	153	2.4	5	925	159	1	OLF8_CHICK	Q98913	gallus gall
853	1	MYG_KOGSI	153	2.4	5	926	159	1	RI1B_ARATH	P42733	arabidopsis
854	1	MYG_LAGLA	153	2.4	5	927	159	1	RI1G_ARATH	O65569	arabidopsis
855	1	MYG_LAGLA	153	2.4	5	928	159	1	RS11_MAIZE	P25460	zea mays (m
856	1	MYG_LEPMU	153	2.4	5	929	159	1	RS11_SOYBN	P17093	glycine max
857	1	MYG_LOXAF	153	2.4	5	930	159	1	YC09_RHILO	Q983b3	rhizobium l
858	1	MYG_LUTLU	153	2.4	5	931	160	1	RI1A_ARATH	P16181	arabidopsis
859	1	MYG_LYCPY	153	2.4	5	932	160	1	RS7_METBU	O93631	methanococc
860	1	MYG_MACRU	153	2.4	5	933	161	1	PRTC_MACMU	Q28506	macaca mula
861	1	MYG_MEGNO	153	2.4	5	934	161	1	SIXA_ECOLI	P76502	eschericchia
862	1	MYG_MELME	153	2.4	5	935	161	1	YA48_SCHPO	Q09727	schizosacch
863	1	MYG_MESCA	153	2.4	5	936	161	1	YD03_MYCTU	Q10619	mycobacteri
864	1	MYG_MOUSE	153	2.4	5	937	161	1	YLAL_BACSU	O07636	bacillus su
865	1	MYG_NYCCO	153	2.4	5	938	162	1	BAR2_CHIPA	P08725	chironomus
866	1	MYG_ONCHP	153	2.4	5	939	162	1	CAB2_BOVIN	Q9n149	bos taurus
867	1	MYG_ONDZP	153	2.4	5	940	162	1	FGFM_MOUSE	Q9ess2	mus musculu
868	1	MYG_ORCOR	153	2.4	5	941	162	1	RI07_HUMAN	P53816	homo sapien
869	1	MYG_ORYAF	153	2.4	5	942	163	1	RI5B_CORAM	O24753	corynebacte
870	1	MYG_PANTR	153	2.4	5	943	163	1	RS10_DROME	Q9vbl4	drosophila
871	1	MYG_PERPO	153	2.4	5	944	163	1	US34_HCMVA	P09709	human cytom
872	1	MYG_PHOPH	153	2.4	5	945	165	1	RIMM_RICPR	Q9zd10	rickettsia
873	1	MYG_PHOSI	153	2.4	5	946	165	1	RS10_XENLA	Q07254	xenopus lae
874	1	MYG_PHYCA	153	2.4	5	947	165	1	YAHC_XENLA	P77219	eschericchia
875	1	MYG_PONPY	153	2.4	5	948	165	1	YG06_YEAST	P53095	saccharomyc
876	1	MYG_PROGU	153	2.4	5	949	166	1	LUXS_HAEIN	P44007	haemophilus
877	1	MYG_RABIT	153	2.4	5	950	166	1	NUOE_ECOLI	P33601	eschericchia
878	1	MYG_ROUAE	153	2.4	5	951	166	1	NUOE_SALTU	P33903	salmonella
879	1	MYG_SHEEP	153	2.4	5	952	166	1	PAL_PSEPU	P43036	pseudomonas
880	1	MYG_SPAEH	153	2.4	5	953	166	1	RL14_DROME	P55841	drosophila
881	1	MYG_TACAC	153	2.4	5	954	166	1	RS10_ICTPU	Q90yr4	ictalurus p
882	1	MYG_TUGPL	153	2.4	5	955	167	1	HPPK_BACSU	P29252	bacillus su
883	1	MYG_TURTR	153	2.4	5	956	167	1	YBL3_FOAMV	P14355	human spuma
884	1	MYG_VULCH	153	2.4	5	957	167	1	YHBS_ECOLI	P45473	eschericchia
885	1	MYG_ZALCA	153	2.4	5	958	167	1	YMW1_YEAST	O04767	saccharomyc
886	1	MYG_ZIPCA	153	2.4	5	959	168	1	LUXS_PASMU	P37901	pasteurella
887	1	FMK1_PSEAE	154	2.4	5	960	168	1	TCPT_SCHPO	Q10344	schizosacch
888	1	INLA_DROME	154	2.4	5	961	168	1	TRIC_CHICK	P27673	gallus gall
889	1	MYG_ALLMI	154	2.4	5	962	168	1	VTU2_DROME	P13238	drosophila
890	1	FGF1_BOVIN	155	2.4	5	963	168	1	YE26_METJA	Q58821	methanococc
891	1	FGF1_CHICK	155	2.4	5	964	169	1	ACPS_THEMA	O9qz56	thermotoga
892	1	FGF1_HUMAN	155	2.4	5	965	169	1	FRBS_BOVIN	P50535	bos taurus
893	1	FGF1_MESAU	155	2.4	5	966	169	1	RGS2_CAEEL	P40908	caenorhabdi
894	1	FGF1_MOUSE	155	2.4	5	967	169	1	ENDA_METTH	O07165	methanobact
895	1	LIPB_PARVE	155	2.4	5	968	170	1	FGFM_HUMAN	P45578	eschericchia
896	1	PCP_YEREN	155	2.4	5	969	170	1	LUXS_ECOLI	Q914t0	salmonella
897	1	RL21_PYUST	155	2.4	5	970	170	1	MSRA_SCHPO	Q09859	schizosacch
898	1	RPB6_YEAST	155	2.4	5	971	171	1	Y77X_HAEIN	O86230	haemophilus
899	1	SLYB_ECOLI	155	2.4	5	972	171	1	ARGR_CORGL	O85175	corynebacte
900	1	SLYB_SALTU	155	2.4	5	973	171	1	FMS1_ECOLI	P25730	eschericchia
901	1	YF45_PSEAE	155	2.4	5	974	171	1	LUXS_VIBHA	Q9z5x1	vibrio harv
902	1	LSPA_BACHD	156	2.4	5	975	171	1	RL10_LACLA	O9c941	lactococcus
903	1	YMS6_CAEEL	156	2.4	5	976	171	1	YCX7_YEAST	P25652	saccharomyc
904	1	YMS6_MYCTU	156	2.4	5	977	171	1	YSNB_BACSU	P94559	bacillus su
905	1	HME_CHICK	157	2.4	5	978	171	1	GLNA_BOVIN	P15103	bos taurus
906	1	LUXS_BORBU	157	2.4	5	979	172	1	IM7B_HUMAN	O60830	homo sapien
907	1	ML14_BRARE	157	2.4	5	980	172	1	PHB1_FREDI	P07119	fremyella d
908	1	PRTC_CANFA	157	2.4	5	981	172	1			
909	1	PRTC_CAPHI	157	2.4	5	982	172	1			

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983 5 2.4 172 1 PHB1_PSEA9 Q52446 pseudanabae
984 5 2.4 172 1 PHB2_PSEA9 Q52451 pseudanabae
985 5 2.4 172 1 PHCB_GALSU P00311 galdieria s
986 5 2.4 172 1 PHCB_MASLA P00310 mastigoclad
987 5 2.4 172 1 PHCB_SPIPL P72508 spirulina p
988 5 2.4 172 1 PHCB_SYNY1 P20777 synechocyst
989 5 2.4 172 1 PHCB_SYNY1 P58060 caulobacter
990 5 2.4 172 1 YD52_SCHPO Q10307 schizosacch
991 5 2.4 173 1 ARPL_DROME Q8xz63 drosophila
992 5 2.4 173 1 CAB5_HUMAN Q9np86 homo sapien
993 5 2.4 173 1 COBP_PSEDE P29p31 pseudomonas
994 5 2.4 173 1 PAL_ECOLI P07176 escherichia
995 5 2.4 173 1 PHB3_FREDI P14877 fremyella d
996 5 2.4 173 1 PHCB_ANASP P70120 anabaena sp
997 5 2.4 173 1 YA92_MYCPN P75600 mycoplasma
998 5 2.4 174 1 RECX_MYCTU O33280 mycobacteri
999 5 2.4 174 1 RUS_HALNI P50558 halobacteri
1000 5 2.4 174 1 VGAM_BPMU P06023 bacterioph
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ALIGNMENTS

```
RESULT 1
FGFK_HUMAN
ID FGFK_HUMAN STANDARD; PRT; 211 AA.
AC Q9NP95;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Fibroblast growth factor-20 (FGF-20).
GN FGF20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20374469; PubMed=10913340;
RA Kirikoshi H., Sagara N., Saitoh T., Tanaka K., Sekihara H.,
RA Shiokawa K., Katoh M.;
RT "Molecular cloning and characterization of human FGF-20 on chromosome
RT 8p21.3-p22.1";
RL Biochem. Biophys. Res. Commun. 274:337-343(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AB044277; BAB03633.1; -.
CC EMBL; AB030648; BAB03530.1; -.
CC MIM; 605558; -.
CC InterPro; IPR002209; HBGFG_FGF.
CC InterPro; IPR002348; ILL_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; ILLHBGF.
CC ProDom; PD000831; HBGFG_FGF; 1.
CC SMART; SM00442; FGF; 1.
CC PROSITE; PS00247; HBGFG_FGF; 1.
CC Growth factor.
SQ SEQUENCE 211 AA; 23498 MW; AB04608C16060CC1 CRC64;
```

Query Match

100.0%; Score 211; DB 1; Length 211;

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Best Local Similarity 100.0%; Pred. No. 2.6e-211;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAPLAEEVGGFGLGGLGQGVGSHFLPPAGERPPLLGERRSAAERSARGPGCAAOIAHL 60
DB 1 MAPLAEEVGGFGLGGLGQGVGSHFLPPAGERPPLLGERRSAAERSARGPGCAAOIAHL 60
QY 61 HGILRRQLYCRTFHQIQLPDGVSQGTQDHSILFGILEFISVAVGLSVIRGVDGSLYL 120
DB 61 HGILRRQLYCRTFHQIQLPDGVSQGTQDHSILFGILEFISVAVGLSVIRGVDGSLYL 120
QY 121 MNDKGLYVSGSKLTSECIFRQPEENWYNYSSNIYKHGDTGRYFVALNKGOTPRDGR 180
DB 121 MNDKGLYVSGSKLTSECIFRQPEENWYNYSSNIYKHGDTGRYFVALNKGOTPRDGR 180
QY 181 SKRHQKTHFLPRVDPDPVPELYKDLMT 211
DB 181 SKRHQKTHFLPRVDPDPVPELYKDLMT 211
RESULT 2
FGF9_XENLA STANDARD; PRT; 209 AA.
AC Q91875;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9) (XFGF-9).
GN FGF9.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97006698; PubMed=8853991;
RA Song J., Slack J.M.W.;
RT "XFGF-9: a new fibroblast growth factor from Xenopus embryos.";
RL Dev. Dyn. 206:427-436(1996).
CC -!- FUNCTION: MAY HAVE A ROLE IN MUSCLE DEVELOPMENT AND NEURAL
CC DIFFERENTIATION, HAS NO SPECIFIC ROLE IN ANTEROPOSTERIOR
CC PATTERNING.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: MATERNAL TRANSCRIPT IS FOUND MAINLY IN THE
CC ANIMAL HEMISPHERE. ZYGOTIC TRANSCRIPT IS FOUND AROUND THE
CC BLASTOPORE AND IN THE LATE GASTRULA STAGE, IN THE DORSAL PART. IN
CC LATER STAGES IT IS FOUND ALONG THE DORSAL PART AND HEAD REGION.
CC -!- DEVELOPMENTAL STAGE: THE MATERNAL PROTEIN IS DETECTED UP TO THE
CC BLASTULA STAGE BUT DECLINES BY THE EARLY GASTRULA. ZYGOTIC
CC EXPRESSION STARTS AT AROUND EARLY GASTRULA; THE LEVEL OF
CC EXPRESSION REACHED AT STAGE 15 PERSISTS DURING NEURULA AND TAILBUD
CC STAGES, AND IS FURTHER INCREASED DURING THE TADPOLE STAGES.
CC -!- PTM: KNOWN TO BE GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
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CC EMBL; U47622; AAC59936.1; -.
CC HSPF; P05230; 2AFC
CC InterPro; IPR002209; HBGFG_FGF.
CC InterPro; IPR002348; ILL_HBGF.
CC Pfam; PF00167; FGF; 1.
CC PRINTS; PR00262; ILLHBGF.
CC ProDom; PD000831; HBGFG_FGF; 1.
CC SMART; SM00442; FGF; 1.
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DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Differentiation; Mitogen; Heparin-binding;
FT PROPEP 1 3 BY SIMILARITY.
FT CHAIN 4 209 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 80 80 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 209 AA; 26CB229797FCBFB CRC64;

Query Match 9.5%; Score 20; DB 1; Length 209;
Best Local Similarity 100.0%; Pred. No. 4e-13; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 139 FREQFEENWNTYSSNIYKH 158
      |||||
Db 137 FREQFEENWNTYSSNIYKH 156

RESULT 3
ID FGF9_HUMAN STANDARD; PRT; 208 AA.
AC P31371;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).
GN FGF9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forekin;
RX MEDLINE=93309459; PubMed=8321227;
RA Miyamoto M., Naruo K.-I., Seko C., Matsumoto S., Kondo T.,
RA Kurokawa T.;
RT "Molecular cloning of a novel cytokine cDNA encoding the ninth member
RT of the fibroblast growth factor family, which has a unique secretion
RT property.";
RT Mol. Cell. Biol. 13:4251-4259(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Blakey S.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 4-26 AND 34-54.
RC TISSUE=Glial tumor;
RX MEDLINE=931515105; PubMed=8428960;
RA Naruo K.-I., Seko C., Kuroshima K.-I., Matsutani E., Sasada R.,
RA Kondo T., Kurokawa T.;
RT "Novel secretory heparin-binding factors from human glioma cells
RT (glia-activating factors) involved in glial cell growth.
RT Purification and biological properties.";
RL J. Biol. Chem. 268:2857-2864(1993).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.60 ANGSTROMS).
RP MEDLINE=21127675; PubMed=11223514;
RA Hecht H.J., Adar R., Hofmann B., Bogin O., Welch H., Yayon A.;
RT "Structure of fibroblast growth factor 9 shows a symmetric dimer with
RT unique receptor- and heparin-binding interfaces.";
RL Acta Crystallogr. D 57:378-384(2001).
CC -1- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLIOSIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: GLIAL CELLS.
CC -1- PTM: THREE MOLECULAR SPECIES WERE FOUND (30 KDA, 29 KDA AND 25
CC KDA), CLEAVED AT LEU-4, VAL-13 AND SER-34 RESPECTIVELY. THE
CC SMALLER ONES MIGHT BE PRODUCTS OF PROTEOLYTIC DIGESTION.
CC FURTHERMORE, THERE MAY BE A FUNCTIONAL SIGNAL SEQUENCE IN THE 30

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CC KDA SPECIES WHICH IS UNCLEAVABLE IN THE SECRETION STEP.
CC -1- PTM: N-GLYCOSYLATED.
CC -1- DISEASE: THE CONTINUOUS OVEREXPRESSION OF GAFS MAY LEAD TO
CC MALIGNANT CELL GROWTH CAUSED BY AN AUTOCRINE LOOP.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -1- DATABASE: NAME=R&D Systems' cytokine source book: FGF9;
CC WWW="http://www.rndsystems.com/asp/q_sitebuilder.asp?bodyID=199".
CC -----
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CC -----
DR EMBL; D14838; BAA03572.1; -.
DR EMBL; AL139378; CAC17692.1; -.
DR PIR; A48137; A48137.
DR PDB; 1G82; 07-MAR-01.
DR MIM; 600921; -.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; ILI_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILI_HBGF.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Differentiation; Mitogen; Heparin-binding;
KW Glycoprotein; 3D-structure.
FT PROPEP 1 3
FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .).
FT CONFLICT 24 26 VLP -> SLL (IN REF. 2).
FT CONFLICT 34 34 S -> A (IN REF. 2).
SQ SEQUENCE 208 AA; 23440 MW; F32A0E7106EF59C9 CRC64;

Query Match 9.0%; Score 19; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.3e-12; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 104 AVGLVSIRGVDSGLYLGNN 122
      |||||
Db 101 AVGLVSIRGVDSGLYLGNN 119

RESULT 4
ID FGF9_MOUSE STANDARD; PRT; 208 AA.
AC P54130;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).
GN FGF9 OR FGF-9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB;
RX MEDLINE=96139512; PubMed=8576175;
RA Santos-Ocampo S., Colvin J.S., Chellaiiah A.T., Ornitz D.M.;
RT "Expression and biological activity of mouse fibroblast growth
RT factor-9.";
RL J. Biol. Chem. 271:1726-1731(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95385801; PubMed=7656983;
RA Seo M., Noguchi K.;
RT "Retinoic acid induces gene expression of fibroblast growth factor-9

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RT during induction of neuronal differentiation of mouse embryonal
RL carcinoma P19 cells.;
RN FEBS Lett. 370:231-235(1995).
RX [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96192599; PubMed=8619928;
RA Hecht D., Zimmerman N., Bedford M., Avivi A., Yayon A.;
RT "Identification of fibroblast growth factor 9 (FGF9) as a high
RT affinity, heparin dependent ligand for FGF receptors 3 and 2 but not
RT for FGF receptors 1 and 4.";
RL Growth Factors 12:223-233(1995).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=J29/SVJ;
RA Colvin J.S., Feldman B., Nadeau J.H., Goldfarb M., Ornitz D.M.;
RT "Genomic organization and embryonic expression of the mouse fibroblast
RT growth factor 9 gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A ROLE IN GLIAL CELL GROWTH AND DIFFERENTIATION
CC DURING DEVELOPMENT, GLIOSIS DURING REPAIR AND REGENERATION OF
CC BRAIN TISSUE AFTER DAMAGE, DIFFERENTIATION AND SURVIVAL OF
CC NEURONAL CELLS, AND GROWTH STIMULATION OF GLIAL TUMORS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC -----
DR EMBL; U3535; AAC52529.1; -
DR EMBL; D38258; BAA07410.1; -
DR EMBL; S82023; AAB36429.1; -
DR EMBL; AF144626; AAD49222.1; -
DR EMBL; AF144624; AAD49222.1; JOINED.
DR EMBL; AF144625; AAD49222.1; JOINED.
DR HSP; P05230; 2AFG.
DR MGD; MGI:104723; Fgf9.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; ILL_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHBGF.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
KW Growth factor; Differentiation; Mitogen; Heparin-binding;
KW Glycoprotein.
FT PROPEP 1 3 BY SIMILARITY.
FT CHAIN 4 208 GLIA-ACTIVATING FACTOR.
FT CARBOHYD 79 79 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 208 AA; 23440 MW; E8DE1EDFE70979E CRC64;

Query Match 9.0%; Score 19; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
Db 101 AVGLVSIRGVDSGLYLGMN 119

RESULT 5
FGF9_RAT
ID FGF9_RAT STANDARD; PRT; 208 AA.
AC F36364;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Glia-activating factor precursor (GAF) (Fibroblast growth factor-9)
DE (FGF-9) (HBGF-9).

Query Match 9.0%; Score 19; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 4.3e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSIRGVDSGLYLGMN 122
Db 101 AVGLVSIRGVDSGLYLGMN 119

RESULT 6
FGFG_HUMAN
ID FGFG_HUMAN STANDARD; PRT; 207 AA.
AC O43320;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-16 (FGF-16).
GN FGF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
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RX MEDLINE=98139883; PubMed=9473496;
RA Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
RA Yamamoto S., Mikami T., Arakawa T., Itoh N.;
RT "Structure and expression of a novel member, FGF-16, on the fibroblast
RT growth factor family.";
RL Biochem. Biophys. Res. Commun. 243:148-152(1998).
CC -1- FUNCTION: INDUCES HEPATOCELLULAR PROLIFERATION. HAS NO BIOLOGICAL
CC EFFECT ON THE HEART (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC -----
DR EMBL; AB009391; BAA24956.1; -.
DR HSSP; P05230; 2AFG.
DR MIM; 603724; -.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; ILI_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHBGF.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR Growth factor.
KW CARBOHYD 78 78 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 207 AA; 23759 MW; D8AD160BDA8DB5F8 CRC64;
SQ
Query Match 7.6%; Score 16; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 GILRRRLQYCRGTGFHL 77
DB 58 GILRRRLQYCRGTGFHL 73
RESULT 7
FGFG_RAT ID FGFG_RAT STANDARD; PRT; 207 AA.
AC OS4769;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fibroblast growth factor-16 (FGF-16).
GN FGF16.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=WISTAR; TISSUE=Heart;
RX MEDLINE=98139883; PubMed=9473496;
RA Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
RA Yamamoto S., Mikami T., Arakawa T., Itoh N.;
RT "Structure and expression of a novel member, FGF-16, on the fibroblast
RT growth factor family.";
RL Biochem. Biophys. Res. Commun. 243:148-152(1998).
CC -1- FUNCTION: INDUCES HEPATOCELLULAR PROLIFERATION. HAS NO BIOLOGICAL
CC EFFECT ON THE HEART. MAY PLAY A ROLE IN THE DEVELOPMENT OF
CC EMBRYONIC BROWN ADIPOSE TISSUE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: IN ADULT, PREDOMINANTLY EXPRESSED IN HEART, IN
CC THE CARDIAC MYOCYTES. NOT DETECTED IN BRAIN, LUNG, LIVER, KIDNEY
CC AND WHITE ADIPOSE TISSUE. IN EMBRYOS, PREDOMINANTLY EXPRESSED IN
CC THE BROWN ADIPOSE TISSUE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IN BROWN ADIPOSE TISSUE DECREASED
CC -----
RX MEDLINE=98139883; PubMed=9473496;
RA Miyake A., Konishi M., Martin F.H., Hernday N.A., Ozaki K.,
RA Yamamoto S., Mikami T., Arakawa T., Itoh N.;
RT "Structure and expression of a novel member, FGF-16, on the fibroblast
RT growth factor family.";
RL Biochem. Biophys. Res. Commun. 243:148-152(1998).
CC -1- FUNCTION: INDUCES HEPATOCELLULAR PROLIFERATION. HAS NO BIOLOGICAL
CC EFFECT ON THE HEART. MAY PLAY A ROLE IN THE DEVELOPMENT OF
CC EMBRYONIC BROWN ADIPOSE TISSUE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: IN ADULT, PREDOMINANTLY EXPRESSED IN HEART, IN
CC THE CARDIAC MYOCYTES. NOT DETECTED IN BRAIN, LUNG, LIVER, KIDNEY
CC AND WHITE ADIPOSE TISSUE. IN EMBRYOS, PREDOMINANTLY EXPRESSED IN
CC THE BROWN ADIPOSE TISSUE.
CC -1- DEVELOPMENTAL STAGE: EXPRESSION IN BROWN ADIPOSE TISSUE DECREASED
CC -----
CC GREATLY AFTER BIRTH.
CC -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
CC -----
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CC -----
DR EMBL; AB002561; BAA24947.1; -.
DR HSSP; P09038; 1BFG.
DR InterPro; IPR002209; HBGF_FGF.
DR InterPro; IPR002348; ILI_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; ILIHBGF.
DR ProDom; PD000831; HBGF_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; 1.
DR Growth factor.
KW CARBOHYD 78 78 N-LINKED (GLCNAC... ) (POTENTIAL).
FT SEQUENCE 207 AA; 23753 MW; IC7A11C8BA3164BC CRC64;
SQ
Query Match 7.6%; Score 16; DB 1; Length 207;
Best Local Similarity 100.0%; Pred. No. 5.6e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 62 GILRRRLQYCRGTGFHL 77
DB 58 GILRRRLQYCRGTGFHL 73
RESULT 8
Y273_METH ID Y273_METH STANDARD; PRT; 151 AA.
AC O26373;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MTH273.
GN MTH273.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanothermobacter.
OX NCBI_TaxID=145262;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougal S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
CC -----
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CC -----
DR EMBL; AE000813; AAB84779.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 151 AA; 16497 MW; 575075BBBC70464E0 CRC64;
```

```
Query Match          3.8%; Score 8; DB 1; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 LPDGSVQG 87
DB 80 LPDGSVQG 87
|||||

RESULT 9
YD58_CAUCR
ID YD58_CAUCR STANDARD; PRT; 157 AA.
AC Q9A8J5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein CCI1358.
GN CCI1358.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.B., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -!- SIMILARITY: BELONGS TO THE UPF0168 FAMILY.
CC
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CC -----
DR EMBL; AE005811; AAK23339.1; -
DR TIGR; CC1358; -
DR InterPro; IPR003796; DUF193.
DR Pfam; PF02644; DUF193; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 157 AA; 17854 MW; 0F1F23C17784614C CRC64;

Query Match          3.8%; Score 8; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 RPVDPERV 200
DB 77 RPVDPERV 84
|||||

RESULT 10
Y665_HUMAN
ID Y665_HUMAN STANDARD; PRT; 756 AA.
AC Q75154; Q9NU10; Q9H1G0; Q9H155;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA0665.
GN KIAA0665.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
TISSUE=Brain;
MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21096910; PubMed=11157797;
RA Daniels R.J., Peden J.F., Lloyd C., Horsley S.W., Clark K.,
RA Tufarelli C., Kearney L., Buckle V.J., Doggett N.A., Flint J.,
RA Higgs D.R.;
RT "Sequence, structure and pathology of the fully annotated terminal 2
RT Mb of the short arm of human chromosome 16.";
RL Hum. Mol. Genet. 10:339-352(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Wallis J., Lloyd C., Hall R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL; AB014565; BAA31640.1; -
DR EMBL; AE006463; AAK61232.1; -
DR EMBL; AL023881; CAC92745.1; -
DR EMBL; AL049542; CAC17519.1; -
DR EMBL; Z98882; CAC17523.1; -
DR InterPro; IPR002048; EF-hand.
DR Pfam; PF00036; ehand; 2.
KW Hypothetical protein; Calcium-binding; Repeat.
FT CA_BIND 215 226 EF-HAND 1 (POTENTIAL).
FT CA_BIND 247 258 EF-HAND 2 (POTENTIAL).
SQ SEQUENCE 756 AA; 82439 MW; 264CEC399F28AFB9 CRC64;

Query Match          3.8%; Score 8; DB 1; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 GPGAAQLA 58
DB 26 GPGAAQLA 33
|||||

RESULT 11
AT2A_HUMAN
ID AT2A_HUMAN STANDARD; PRT; 1047 AA.
AC Q75110; Q9NQK6; Q9NQK7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Potential phospholipid-transporting ATPase IIA (EC 3.6.1.-).
GN ATP9A OR KIAA0611.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
TISSUE=Brain;
RP SEQUENCE OF 15-1047 FROM N.A. (SHORT ISOFORM).
RX MEDLINE=98403880; PubMed=9734811;
```

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.U.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gillman R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levaslaiho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
 RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 CC -|- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -|- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING
 CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
 CC ATPASES). SUBFAMILY IV.
 CC -----
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 CC -----
 DR EMBL; AB014511; BAA31586.1; -
 DR EMBL; AL335379; CAC17554.1; -
 DR EMBL; AL138807; CAB92773.1; -
 DR EMBL; AL035684; CAB63450.1; -
 DR EMBL; AL138807; CAB92774.1; ALT_SEQ.
 DR InterPro: IPR001757; E1-E2_ATPase.
 DR Pfam: PF00702; Hydrolase; 1.
 DR PROSITE: PR00119; CATATPASE
 DR PROSITE: PS00154; ATPASE_E1E2; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 KW Alternative splicing; Multigene family.
 FT DOMAIN 1 69
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 70 91
 FT POTENTIAL.
 FT DOMAIN 92 96
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 97 119
 FT POTENTIAL.
 FT DOMAIN 120 303
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 304 325
 FT POTENTIAL.
 FT DOMAIN 326 332
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 333 354
 FT POTENTIAL.
 FT DOMAIN 355 841
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 842 862
 FT POTENTIAL.
 FT DOMAIN 863 874
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 875 893
 FT POTENTIAL.
 FT DOMAIN 894 923
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 924 942
 FT POTENTIAL.
 FT DOMAIN 943 949
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 950 972
 FT POTENTIAL.
 FT DOMAIN 973 978
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 979 999
 FT POTENTIAL.
 FT DOMAIN 1000 1006
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1007 1030
 FT POTENTIAL.
 FT DOMAIN 1031 1047
 FT CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 391 391
 FT PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 785 785
 FT MAGNESIUM (BY SIMILARITY).
 FT METAL 789 789
 FT MAGNESIUM (BY SIMILARITY).
 FT VARSPLIC 149 269
 FT MISSING (IN SHORT ISOFORM).
 SQ SEQUENCE 1047 AA; 118582 MW; 80C307CF5A396755 CRC64;
 Query Match 3.8%; Score 8; DB 1; Length 1047;
 Best Local Similarity 100.0%; Pred. No. 4.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 201 PELYKDLL 208
 Db 907 PELYKDLL 914
 RESULT 12
 AT9A_MOUSE
 ID AT9A_MOUSE STANDARD; PRT; 1047 AA.
 AC 070228;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotating update)
 DE Potential phospholipid-transporting ATPase IIA (EC 3.6.3.1).
 GN ATP9A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20473714; PubMed=11015572;
 RA Halleck M.S., Lawler J.F. Jr., Blackshaw S., Gao L., Nagarajan P.,
 RA Hacker C., Pyle S., Newman J.T., Nakanishi Y., Ando H., Weinstock D.,
 RA Williamson P., Schlegel R.A.;
 RT "Differential expression of putative transbilayer amphipath
 RT transporters.";
 RL Physiol. Genomics 1:139-150(1999).
 RN [2]
 RP SEQUENCE OF 28-1047 FROM N.A.
 RX MEDLINE=98217376; PubMed=9548971;
 RA Halleck M.S., Pradhan D., Blackman C.F., Berkes C., Williamson P.L.,
 RA Schlegel R.A.;
 RT "Multiple members of a third subfamily of P-type ATPases identified by
 RT genomic sequences and ESTs.";
 RL Genome Res. 8:354-361(1998).
 CC -|- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + PHOSPHATE.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -|- TISSUE SPECIFICITY: FOUND IN MOST TISSUES EXCEPT SPLEEN. MOST
 CC ABUNDANT IN BRAIN. ALSO DETECTED IN FETAL TISSUES.
 CC -|- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
 CC ATPASES). SUBFAMILY IV.
 CC -----
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 CC -----
 DR EMBL; AF152243; AAF08396.1; -
 DR EMBL; AF011336; AAC05245.1; -

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DR MGD; MGI:1330826; Atp9a.
DR InterPro; IPR001757; E1-E2_ATPase.
DR InterPro; IPR001454; Hydrolase.
DR Pfam; PF00702; Hydrolase; 1.
DR PRINTS; PR001119; CATAPASE.
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
KW Multigene family.
FT DOMAIN 1 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 91 POTENTIAL.
FT DOMAIN 92 96 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 97 119 POTENTIAL.
FT DOMAIN 120 303 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 304 325 POTENTIAL.
FT DOMAIN 326 332 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 333 354 POTENTIAL.
FT DOMAIN 355 841 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 842 862 POTENTIAL.
FT DOMAIN 863 874 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 875 893 POTENTIAL.
FT DOMAIN 894 923 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 924 942 POTENTIAL.
FT DOMAIN 943 949 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 950 972 POTENTIAL.
FT DOMAIN 973 978 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 979 999 POTENTIAL.
FT DOMAIN 1000 1006 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1007 1030 POTENTIAL.
FT DOMAIN 1031 1047 CYTOPLASMIC (POTENTIAL).
FT MOD_RES 391 785 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 785 789 MAGNESIUM (BY SIMILARITY).
FT METAL 789 789 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 29 29 R -> K (IN REF. 2).
FT CONFLICT 129 129 V -> I (IN REF. 2).
FT CONFLICT 138 138 V -> I (IN REF. 2).
FT CONFLICT 138 138 R -> K (IN REF. 2).
FT CONFLICT 278 278 Q -> P (IN REF. 2).
FT CONFLICT 432 432 S -> C (IN REF. 2).
FT CONFLICT 475 475 V -> I (IN REF. 2).
FT CONFLICT 533 533 H -> D (IN REF. 2).
FT CONFLICT 613 613 E -> D (IN REF. 2).
FT CONFLICT 742 742 W -> G (IN REF. 2).
FT CONFLICT 784 784 W -> G (IN REF. 2).
SQ SEQUENCE 1047 AA; 118756 MW; B76AE98C32F6D04 CRC64;

Query Match 3.8%; Score 8; DB 1; Length 1047;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PELYKDIL 208
Db 907 PELYKDIL 914
|||||||

RESULT 13
ID THFB_HAEIN STANDARD; PRT; 94 AA.
AC P43724;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Integration host factor beta-subunit (IHF-beta).
GN IHFB OR HIMD OR H1221.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OC NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

RA Scott J.D., Shirley R., Liu L.-I., Glodex A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE TWO SUBUNITS OF INTEGRATION
CC HOST FACTOR, A SPECIFIC DNA-BINDING PROTEIN THAT FUNCTIONS IN
CC GENETIC RECOMBINATION AS WELL AS IN TRANSCRIPTIONAL AND
CC TRANSLATIONAL CONTROL (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL HISTONE-LIKE PROTEIN FAMILY.
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CC -----
CC EMBL; U32802; AAC22874.1; -
CC HSSP; P08756; 1IHF.
DR TIGR; H1221; -.
DR InterPro; IPR000119; Bac_DNA_binding.
DR Pfam; PF00216; Bac_DNA_binding; 1.
DR ProDom; PD000945; Bac_DNA_binding; 1.
DR SMART; SM00411; BHL; 1.
DR PROSITE; PS00045; HISTONE_LIKE; 1.
DR DNA-binding; Transcription regulation; DNA recombination;
KW Translation regulation; Complete proteome.
SQ SEQUENCE 94 AA; 10454 MW; 3EAA97B915B63EAF CRC64;

Query Match 3.3%; Score 7; DB 1; Length 94;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 96 GILEFIS 102
Db 28 GILEFIS 34
|||||||

RESULT 14
ID CEPL_CERFI STANDARD; PRT; 120 AA.
AC P81702;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cerato-platanin.
OS Ceratocystis fimbriata f. sp. platani.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Microascales; Microasaceae; Ceratocystis.
OX NCBI_TaxID=88771;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND DISULFIDE BONDS.
RC STRAIN=AF 100;
RX MEDLINE=99386981; PubMed=10455173;
RA Pazzagli L., Cappugi G., Manso G., Camici G., Santini A.,
RA Scala A.;
RT "Purification, characterization, and amino acid sequence of cerato-
RT platanin, a new phytotoxic protein from Ceratocystis fimbriata f.sp.
RT platani.";
RL J. Biol. Chem. 274:24959-24964(1999).
CC -!- FUNCTION: PHYTOXIN WHICH CAUSES PRODUCTION OF PHYTOALEXIN IN
CC PLATANUS ACERIFOLIA, PLATANUS OCCIDENTALIS AND PLATANUS
CC ORIENTALIS. INDUCES ALSO CELL NECROSIS. BEHAVES AS FUNGAL TOXIN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=12383.6.; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE CERATO-PLATANIN FAMILY.
CC -----
```

```
KW Toxin.
FT DISULFID 20 57
FT DISULFID 60 115
SQ SEQUENCE 120 AA; 12400 MW; 131E727B02626B48 CRC64;

Query Match 3.3%; Score 7; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 IRGVDSG 116
Db 73 IRGVDSG 79

RESULT 15
GLB1_LUMTE STANDARD; PRT; 142 AA.
AC P08924; 1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DE Globin I, extracellular (Erythrocyte) (Globin D).
OS Lumbricus terrestris (Common earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Lumbricus.
OX NCBI_TaxID=6398;
RN [1]
RP SEQUENCE.
RX MEDLINE=87137584; PubMed=3546301;
RA Shishikura F., Snow J.W., Gotoh T., Vinogradov S.N., Walz D.A.;
RT "Amino acid sequence of the monomer subunit of the extracellular
hemoglobin of Lumbricus terrestris."
RL J. Biol. Chem. 262:3123-3131(1987).
CC -!- SUBUNIT: THE EXTRACELLULAR HEMOGLOBIN OF THE EARTHWORM CONSISTS
OF 12 SUBUNITS THAT HAVE A HEXAGONAL BILAYER STRUCTURE WITH A
MOLECULAR WEIGHT NEAR 3.8 MILLION. EACH ONE-TWELFTH SUBUNIT IS
COMPOSED PRIMARILY OF DISULFIDE LINKED TRIMERS (CHAINS A, B,
AND C) AND MONOMERS (CHAIN D).
CC -!- SIMILARITY: TO OTHER WORM GLOBIN SUBUNITS.
DR PIR; A29134; A29134.
DR InterPro; IPR002336; Erythruin.
DR InterPro; IPR000971; Globin.
DR Pfam; PF00042; globin; 1.
DR PRINTS; PR00611; ERYTHRUORIN.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT DISULFID 2 131 BY SIMILARITY
SQ SEQUENCE 142 AA; 16129 MW; 87BE8C74D1BBF1BE CRC64;

Query Match 3.3%; Score 7; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 AAQLAHL 60
Db 84 AAQLAHL 90

Search completed: October 21, 2002, 16:20:14
Job time : 52 secs
```


GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: October 21, 2002, 16:16:01 ; Search time 29 Seconds
(without alignments)
1258.687 Million cell updates/sec

Title: US-09-817-814-2
Perfect score: 211
Sequence: 1 MAPLAEVGGFLGLEGLGQQ.....PRPVDPERVPELYKDLLMYT 211

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_19.*

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp-invertebrate.*
- 6: sp-mammal.*
- 7: sp-mhc.*
- 8: sp-organelle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp-unclassified.*
- 15: sp-rvirus.*
- 16: sp-bacteriaph.*
- 17: sp-archae.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	40.3	212	11 Q9EST9	Q9est9 rattus norv
2	75	35.5	212	11 Q9ESL9	Q9esl9 mus musculus
3	26	12.3	208	13 Q9PY1	Q9py1 xenopus lae
4	19	9.0	208	6 Q9SL12	Q9sl12 sus scrofa
5	16	7.6	207	11 Q9ESL8	Q9esl8 mus musculus
6	16	7.6	207	11 Q9ERQ5	Q9erq5 mus musculus
7	8	3.8	197	10 Q9S9P9	Q9s9p9 arabidopsis
8	8	3.8	215	10 Q9M607	Q9m607 vitis ripar
9	8	3.8	226	10 Q64585	Q64585 arabidopsis
10	8	3.8	275	11 Q70128	Q70128 rattus norv
11	8	3.8	545	10 Q9M332	Q9m332 arabidopsis
12	8	3.8	564	2 Q9X2Y5	Q9x2y5 bacillus an
13	8	3.8	964	10 Q922L9	Q922l9 mus musculus
14	7	3.3	70	16 Q9KCM8	Q9kcw8 bacillus ha
15	7	3.3	101	16 Q9PE80	Q9pe80 xylella fas
16	7	3.3	116	2 Q9SLY6	Q9sly6 streptomyce

Q96mi2	homo sapien	17	3.3	128	4	Q96MI2
Q91090	streptomyce	18	3.3	146	2	Q9LO90
Q9k4k1	streptomyce	19	3.3	148	2	Q9K4K1
Q919r6	pectobacter	20	3.3	149	2	Q9L9R6
Q9nv89	homo sapien	21	3.3	158	4	Q9NV89
Q61233	lumbricus t	22	3.3	158	5	Q61233
Q61234	lumbricus t	23	3.3	158	5	Q61234
Q99yl7	streptococc	24	3.3	160	16	Q99YL7
Q97nu6	streptococc	25	3.3	167	16	Q97NU6
Q97614	sulfolobus	26	3.3	168	17	Q97614
Q9evb4	streptococc	27	3.3	170	2	Q9EVB4
Q9kut4	vibrio chol	28	3.3	177	16	Q9KUT4
Q9fpp1	amphidinium	29	3.3	188	10	Q9FPP1
Q9axm8	amphidinium	30	3.3	188	10	Q9AXM8
Q9dqp9	human immun	31	3.3	206	15	Q9DQP9
Q97962	human immun	32	3.3	209	15	Q97962
Q84742	chlamydia t	33	3.3	219	16	Q84742
Q9pli9	chlamydia m	34	3.3	219	16	Q9PLI9
Q9ji98	mus musculus	35	3.3	232	11	Q9Ji98
Q19985	arabidopsis	36	3.3	236	8	Q19985
Q81717	arabidopsis	37	3.3	236	10	Q81717
Q49915	oryza sativ	38	3.3	238	10	Q49915
Q9ft78	arabidopsis	39	3.3	241	10	Q9FT78
Q9c239	neutrospora	40	3.3	246	3	Q9C239
Q69083	human herpe	41	3.3	250	12	Q69083
Q9zbe6	mycobacteri	42	3.3	251	16	Q9ZBE6
Q53033	rhodospirill	43	3.3	255	2	Q53033
Q81288	arabidopsis	44	3.3	262	10	Q81288
Q9ycr5	aeropyrum p	45	3.3	267	17	Q9YCR5
Q33182	mycobacteri	46	3.3	274	16	Q33182
Q91105	pseudomonas	47	3.3	278	16	Q91105
Q986u9	rhizobium l	48	3.3	298	16	Q986U9
Q9ae56	rhodococcus	49	3.3	304	2	Q9AE56
Q91183	streptomyce	50	3.3	312	2	Q91183
Q93qz0	clostridium	51	3.3	312	2	Q93QZ0
P74157	synecocyst	52	3.3	314	16	P74157
Q9nt28	homo sapien	53	3.3	316	4	Q9NT28
Q17822	caenorhabdl	54	3.3	316	5	Q17822
Q9ha72	homo sapien	55	3.3	323	4	Q9HA72
Q9f3z8	neisseria m	56	3.3	329	2	Q9F3Z8
Q9p45	jonopsidium	57	3.3	330	16	Q9P45
Q9sp44	jonopsidium	58	3.3	381	10	Q9SP44
Q9k7z6	bacillus ha	59	3.3	387	16	Q9K7Z6
Q83618	mumps virus	60	3.3	388	16	Q83618
Q9dqa3	mumps virus	61	3.3	391	12	Q9DQA3
Q9416	mumps virus	62	3.3	391	12	Q9J4L6
Q910s3	mumps virus	63	3.3	391	12	Q910S3
Q67276	aquifex aeo	64	3.3	392	16	Q67276
Q60198	escherichia	65	3.3	400	2	Q60198
Q9uhro	homo sapien	66	3.3	414	4	Q9UHR0
Q9hbh8	homo sapien	67	3.3	414	4	Q9HBH8
Q41607	human immun	68	3.3	418	15	Q41607
Q41608	human immun	69	3.3	418	15	Q41608
Q9x6e1	photobacter	70	3.3	420	2	Q9X6E1
Q76831	caenorhabdl	71	3.3	425	5	Q76831
Q91i13	mus musculus	72	3.3	427	11	Q99LI3
Q9klq8	vibrio chol	73	3.3	436	16	Q9KLQ8
Q9ycw5	aeropyrum p	74	3.3	439	17	Q9YCW5
P94647	chlorobium	75	3.3	474	2	P94647
Q53032	rhodospirill	76	3.3	480	2	Q53032
Q9a595	caulobacter	77	3.3	486	16	Q9A595
Q9988	herpes simp	78	3.3	486	12	Q9988
Q97kc0	clostridium	79	3.3	492	16	Q97KC0
Q9j0x9	human herpe	80	3.3	512	12	Q9J0X9
Q92pp7	rhizobium m	81	3.3	549	16	Q92PP7
Q64069	bacterioph	82	3.3	559	9	Q64069
Q31952	bacillus su	83	3.3	589	16	Q31952
Q9fbis	streptomyce	84	3.3	593	2	Q9FBI5
Q921u9	mus musculus	85	3.3	626	11	Q921U9
Q9w556	drosophila	86	3.3	631	5	Q9W556
Q9h8h9	homo sapien	87	3.3	637	4	Q9H8H9
Q93gz5	streptomyce	88	3.3	641	2	Q93GZ5

90	7	3.3	657	10	023427	023427 arabidopsis	163	6	2.8	82	12	09YJ13	09YJ13 encephalomy
91	7	3.3	676	13	Q9DCG7	Q9dgc7 brachydanio	164	6	2.8	82	12	Q9WK34	Q9wk34 encephalomy
92	7	3.3	678	5	Q9V3Q6	Q9v3q6 drosophila	165	6	2.8	82	12	Q9WK33	Q9wk33 encephalomy
93	7	3.3	703	2	Q9L3P4	Q9l3p4 uncultured	166	6	2.8	82	12	Q9YPK8	Q9ypk8 encephalomy
94	7	3.3	711	4	Q9H123	Q9h123 homo sapien	167	6	2.8	82	12	Q9YPK7	Q9ypk7 encephalomy
95	7	3.3	711	4	Q9K125	Q9k125 homo sapien	168	6	2.8	82	12	Q9YPK5	Q9ypk5 encephalomy
96	7	3.3	711	4	Q9K124	Q9k124 homo sapien	169	6	2.8	84	12	Q9LEQ2	Q9leq2 dengue viru
97	7	3.3	738	10	Q9M0Z0	Q9m0z0 arabidopsis	170	6	2.8	86	16	Q97LR6	Q97lk6 clostridium
98	7	3.3	743	10	Q93V99	Q93v99 arabidopsis	171	6	2.8	88	2	Q9S590	Q9s590 nitrosomona
99	7	3.3	757	5	Q9UFA2	Q9ufa2 homo sapien	172	6	2.8	88	15	Q9WCP3	Q9wcp3 human immun
100	7	3.3	757	5	Q960E5	Q960e5 drosophila	173	6	2.8	89	4	Q16343	Q16343 homo sapien
101	7	3.3	772	10	Q9ZPH7	Q9zph7 arabidopsis	174	6	2.8	90	10	Q9ZVC5	Q9zvc5 arabidopsis
102	7	3.3	782	5	Q9N1S1	Q9n1s1 drosophila	175	6	2.8	90	17	Q97CT1	Q97ct1 thermoplasm
103	7	3.3	783	5	Q9VF04	Q9vf04 drosophila	176	6	2.8	90	17	Q97I24	Q97i24 sulfolobus
104	7	3.3	812	2	Q9FBT4	Q9fbt4 streptomyce	177	6	2.8	91	5	Q9NBJ9	Q9nbj9 caenorhabdi
105	7	3.3	815	2	Q93740	Q93740 rhodobacter	178	6	2.8	91	17	Q9UY47	Q9uy47 pyrococcus
106	7	3.3	829	16	Q9K1R4	Q9k1r4 vibrio chol	179	6	2.8	93	12	Q98335	Q98335 macroptiliu
107	7	3.3	829	16	Q9K1G3	Q9k1g3 pseudomonas	180	6	2.8	95	12	Q98443	Q98443 paramecium
108	7	3.3	831	2	Q98111	Q98111 rhodobacter	181	6	2.8	95	15	Q99DE3	Q99de3 human immun
109	7	3.3	834	2	Q9Z3W4	Q9z3w4 pseudomonas	182	6	2.8	96	10	Q41900	Q41900 arabidopsis
110	7	3.3	834	16	Q9Z236	Q9z236 rhizobium m	183	6	2.8	96	15	Q9DHC0	Q9dhc0 human immun
111	7	3.3	853	2	Q9RC05	Q9rc05 pseudomonas	184	6	2.8	96	15	Q9DHA6	Q9dha6 human immun
112	7	3.3	875	16	Q9Z2R5	Q9z2tm5 rhizobium m	185	6	2.8	96	15	Q9DH59	Q9dh59 human immun
113	7	3.3	917	4	Q9H698	Q9h698 homo sapien	186	6	2.8	96	15	Q9E519	Q9e519 human immun
114	7	3.3	917	4	Q96F81	Q96f81 homo sapien	187	6	2.8	97	2	Q9F5E1	Q9f5el agrobacteri
115	7	3.3	955	4	Q96DN2	Q96dn2 homo sapien	188	6	2.8	97	2	Q930Y5	Q930y5 agrobacteri
116	7	3.3	1012	5	Q76903	Q76903 drosophila	189	6	2.8	97	15	Q99DD3	Q99dd3 human immun
117	7	3.3	1025	2	Q54507	Q54507 streptococc	190	6	2.8	98	2	Q9BXH1	Q9bxh1 streptomyce
118	7	3.3	1025	2	P72532	P72532 streptococc	191	6	2.8	98	4	Q9BZH7	Q9bzh7 homo sapien
119	7	3.3	1058	5	Q9VK04	Q9vk04 drosophila	192	6	2.8	98	10	Q9XFT7	Q9xft7 chlamydomon
120	7	3.3	1058	16	Q930F6	Q930f6 rhizobium m	193	6	2.8	99	3	Q9C225	Q9c225 neurospora
121	7	3.3	1120	5	Q9VUK6	Q9vuk6 drosophila	194	6	2.8	99	10	Q9ZVC4	Q9zvc4 arabidopsis
122	7	3.3	1152	3	Q9UUY1	Q9uuy1 neurospora	195	6	2.8	100	16	Q9MFD1	Q9mfd1 beta vulgar
123	7	3.3	1267	13	Q98945	Q98945 gallus gall	196	6	2.8	100	16	Q98DK6	Q98dk6 rhizobium l
124	7	3.3	1326	2	Q9L2C3	Q9l2c3 streptomyce	197	6	2.8	100	17	Q9YD29	Q9yvd29 aeropyrum p
125	7	3.3	1331	3	Q9HED0	Q9hed0 neurospora	198	6	2.8	101	2	Q9R413	Q9r413 ureaplasma
126	7	3.3	1339	4	Q75276	Q75276 homo sapien	199	6	2.8	101	2	Q9R7K9	Q9r7k9 ureaplasma
127	7	3.3	1418	16	Q9RRW1	Q9rrw1 deinococcus	200	6	2.8	101	2	Q9R7K8	Q9r7k8 ureaplasma
128	7	3.3	1530	5	Q9NH11	Q9nh11 drosophila	201	6	2.8	101	2	Q9R7K7	Q9r7k7 ureaplasma
129	7	3.3	1536	3	Q96625	Q96625 saccharomyc	202	6	2.8	101	2	Q9R7K6	Q9r7k6 ureaplasma
130	7	3.3	1536	3	Q93808	Q93808 saccharomyc	203	6	2.8	101	2	Q9R7K5	Q9r7k5 ureaplasma
131	7	3.3	1579	5	Q9VSE6	Q9vse6 drosophila	204	6	2.8	101	2	Q9R7K4	Q9r7k4 ureaplasma
132	7	3.3	1581	4	Q94911	Q94911 homo sapien	205	6	2.8	101	2	Q9R7K3	Q9r7k3 ureaplasma
133	7	3.3	1607	5	Q94599	Q94599 leishmania	206	6	2.8	101	2	Q9R7K2	Q9r7k2 ureaplasma
134	7	3.3	1778	5	Q9NE65	Q9ne65 leishmania	207	6	2.8	101	2	Q9R7K2	Q9r7k2 ureaplasma
135	7	3.3	2163	5	Q91912	Q91912 caenorhabdi	208	6	2.8	101	2	Q93336	Q93336 alcaligenes
136	7	3.3	3390	12	Q99D35	Q99d35 dengue viru	209	6	2.8	101	2	Q93T82	Q93t82 brucella ab
137	7	3.3	3638	4	Q15142	Q15142 homo sapien	210	6	2.8	101	8	Q9BAC0	Q9bac0 euglena ste
138	7	3.3	4292	4	Q15141	Q15141 homo sapien	211	6	2.8	101	10	Q94LA6	Q94la6 arabidopsis
139	7	3.3	4302	4	Q15140	Q15140 homo sapien	212	6	2.8	101	17	Q97ZL0	Q97z10 sulfolobus
140	7	3.3	13055	5	Q9165	Q9165 caenorhabdi	213	6	2.8	103	2	Q9Z376	Q9z376 actinomycetes
141	6	2.8	22	2	Q9R5C0	Q9r5c0 nitrosomona	214	6	2.8	103	10	Q9SYR2	Q9syrr2 urtica diol
142	6	2.8	27	10	Q9S8M4	Q9s8m4 avena sativ	215	6	2.8	105	2	Q9RZW7	Q9rzw7 borrelia bu
143	6	2.8	49	12	Q91FK3	Q91fk3 chilo iride	216	6	2.8	106	2	Q97401	Q97401 synchococc
144	6	2.8	51	4	Q9UJ11	Q9uj11 homo sapien	217	6	2.8	106	4	Q9UN93	Q9un93 homo sapien
145	6	2.8	61	16	Q92WL2	Q92wl2 rhizobium m	218	6	2.8	106	16	Q92H48	Q92h48 rickettsia
146	6	2.8	64	10	Q42983	Q42983 oryza sativ	219	6	2.8	107	10	Q64841	Q64841 arabidopsis
147	6	2.8	64	16	Q9PD64	Q9pd64 xyliella fas	220	6	2.8	108	11	Q9D2X4	Q9d2x4 mus musculu
148	6	2.8	65	2	Q47784	Q47784 enterococcu	221	6	2.8	108	15	Q9QN68	Q9qn68 human immun
149	6	2.8	65	2	Q91658	Q91658 enterococcu	222	6	2.8	108	15	Q10826	Q10826 human immun
150	6	2.8	66	11	Q9Z5P4	Q9z5p4 mus musculu	223	6	2.8	111	2	Q9FBX9	Q9fbx9 streptomyce
151	6	2.8	67	2	Q54576	Q54576 streptococc	224	6	2.8	111	2	Q9ACQ0	Q9acq0 streptomyce
152	6	2.8	68	2	Q83015	Q83015 streptomyce	225	6	2.8	111	12	Q85304	Q85304 orf viru
153	6	2.8	70	7	Q95194	Q95194 stizostedio	226	6	2.8	112	2	Q9R1W3	Q9r1w3 streptomyce
154	6	2.8	70	7	Q95192	Q95192 stizostedio	227	6	2.8	112	10	Q9S7W3	Q9s7w3 urtica diol
155	6	2.8	70	7	Q95191	Q95191 stizostedio	228	6	2.8	112	10	Q9S7K1	Q9s7k1 urtica diol
156	6	2.8	70	7	Q95188	Q95188 stizostedio	229	6	2.8	112	10	Q9S7B3	Q9s7b3 urtica diol
157	6	2.8	70	7	Q95183	Q95183 stizostedio	230	6	2.8	112	10	Q9S705	Q9s705 urtica diol
158	6	2.8	78	10	Q9M5K8	Q9m5k8 zea mays (m	231	6	2.8	112	10	Q9ZP51	Q9zps1 urtica diol
159	6	2.8	78	9	Q94MY7	Q94my7 haemophilus	232	6	2.8	112	10	Q9SPR5	Q9spr5 urtica diol
160	6	2.8	82	12	Q9YJ99	Q9yj99 encephalomy	233	6	2.8	112	15	Q75730	Q75730 human immun
161	6	2.8	82	12	Q9YJ06	Q9yj06 encephalomy	234	6	2.8	112	15	Q75731	Q75731 human immun
162	6	2.8	82	12	Q9YJMI	Q9yjmi encephalomy	235	6	2.8	112	17	Q972S1	Q972s1 sulfolobus

236	113	10	Q9S7C2	Q9S7C2 urtica dioi	309	6	2.8	146	16	Q92X66	Q92X66 rhizobium m
237	114	10	Q9AST5	Q9ast5 arabidopsis	310	6	2.8	148	12	Q9YLA6	Q9yla6 macrophilia
238	115	2	Q00605	Q00605 streptococc	311	6	2.8	148	17	Q9V252	Q9v252 pyrococcus
239	115	15	Q97005	Q97005 human immun	312	6	2.8	149	2	Q9L9T5	Q9l9t5 brenneria r
240	116	11	Q9D3K8	Q9d3k8 mus musculu	313	6	2.8	149	2	Q9L9T3	Q9l9t3 brenneria r
241	116	15	Q70199	Q70199 human immun	314	6	2.8	149	2	Q9L9T2	Q9l9t2 brenneria r
242	116	15	O40241	O40241 human immun	315	6	2.8	149	2	Q9R1I1	Q9r1i1 yersinia pe
243	116	15	O40242	O40242 human immun	316	6	2.8	149	5	Q25383	Q25383 loligo peal
244	116	15	Q97007	Q97007 human immun	317	6	2.8	149	12	P88975	P88975 macrophilia
245	117	2	Q9F8Z8	Q9f8z8 streptococc	318	6	2.8	151	12	P88893	P88893 jamaican to
246	117	16	Q99T85	Q99t85 staphylococ	319	6	2.8	152	8	O48119	O48119 ungaliophis
247	118	8	Q35595	Q35595 physarum po	320	6	2.8	152	15	Q9DRS6	Q9drs6 human immun
248	118	15	O41584	O41584 human immun	321	6	2.8	152	16	Q9A2T9	Q9a2t9 caulobacter
249	120	15	O41592	O41592 human immun	322	6	2.8	153	2	Q9EWY1	Q9ewy1 streptomyc
250	121	11	Q99LY5	Q99ly5 mus musculu	323	6	2.8	153	10	Q9LW8	Q9lw8 oryza sativ
251	121	15	Q76348	Q76348 human immun	324	6	2.8	153	12	O41475	O41475 weissadula g
252	121	15	Q97866	Q97866 human immun	325	6	2.8	153	15	Q74916	Q74916 human immun
253	121	17	Q9YAA1	Q9yaal aeropyrum p	326	6	2.8	153	16	Q982G4	Q982g4 rhizobium l
254	122	4	Q9UFS1	Q9ufsi homo sapien	327	6	2.8	154	11	Q63847	Q63847 mus musculu
255	122	5	Q9TYV6	Q9tyv6 caenorhabdi	328	6	2.8	154	15	P88419	P88419 human immun
256	122	6	Q95KC2	Q95kc2 macaca fasc	329	6	2.8	155	2	O85238	O85238 yersinia en
257	123	2	Q50766	Q50766 mycobacteri	330	6	2.8	155	15	P88431	P88431 human immun
258	123	15	Q9QM82	Q9qm82 human immun	331	6	2.8	157	15	Q9Q5H0	Q9q5h0 human immun
259	123	15	Q85587	Q85587 aids-associ	332	6	2.8	157	15	Q9Q5G9	Q9q5g9 human immun
260	124	11	Q9D179	Q9d179 mus musculu	333	6	2.8	159	5	Q9BHK1	Q9bhl1 sabella spa
261	124	13	Q90XQ5	Q90xq5 ambystoma m	334	6	2.8	159	8	Q9MG06	Q9mg06 haemoproteu
262	124	16	Q9KG60	Q9kg60 bacillus ha	335	6	2.8	159	8	Q9MG05	Q9mg05 haemoproteu
263	125	6	Q95K85	Q95k85 macaca fasc	336	6	2.8	159	8	Q9MG04	Q9mg04 haemoproteu
264	129	4	Q43180	Q43180 homo sapien	337	6	2.8	159	8	Q9MG03	Q9mg03 haemoproteu
265	129	4	Q96MT5	Q96mt5 homo sapien	338	6	2.8	159	8	Q9MG02	Q9mg02 haemoproteu
266	129	11	Q9CVD0	Q9cvd0 mus musculu	339	6	2.8	159	8	Q9MG01	Q9mg01 haemoproteu
267	129	15	Q9QRB0	Q9qrb0 human immun	340	6	2.8	159	8	Q9MG00	Q9mg00 haemoproteu
268	130	2	Q50753	Q50753 mycobacteri	341	6	2.8	159	8	Q9MEZ7	Q9mfz7 haemoproteu
269	131	2	Q9A1K9	Q9aik9 pseudomonas	342	6	2.8	159	8	Q9MEZ4	Q9mfz4 haemoproteu
270	131	5	Q9V5V5	Q9vsv5 pseudophila	343	6	2.8	159	10	Q9F6Z2	Q9fz2 arabidopsis
271	131	17	Q9YBW3	Q9ybw3 aeropyrum p	344	6	2.8	160	16	Q97SJ9	Q97sj9 streptococ
272	132	10	Q9FWG9	Q9fwg9 oryza sativ	345	6	2.8	161	2	Q9RWA8	Q9rma8 bacillus ci
273	132	10	Q9FU43	Q9fu43 oryza sativ	346	6	2.8	162	12	O09723	O09723 bean golden
274	132	12	Q91EQ7	Q91eq7 dengue viru	347	6	2.8	162	15	Q9WIR1	Q9wir1 human immun
275	132	12	Q91E06	Q91eq6 dengue viru	348	6	2.8	162	15	Q9WIR3	Q9wir3 human immun
276	132	12	Q91EQ5	Q91eq5 dengue viru	349	6	2.8	163	17	Q9V1I9	Q9v1i9 pyrococcus
277	132	12	Q91EQ4	Q91eq4 dengue viru	350	6	2.8	164	4	Q9NSJ2	Q9nsj2 homo sapien
278	132	12	Q91EQ3	Q91eq3 dengue viru	351	6	2.8	164	16	Q9AB51	Q9ab51 caulobacter
279	133	8	Q36308	Q36308 adalia bipu	352	6	2.8	165	2	Q9K3X8	Q9k3x8 streptomyc
280	133	16	O07760	O07760 mycobacteri	353	6	2.8	165	5	Q966T8	Q966t8 bombyx mori
281	134	2	Q9XB26	Q9xb26 klebsiella	354	6	2.8	165	17	Q9YE68	Q9ye68 aeropyrum p
282	134	12	Q9QD36	Q9qdj6 tomato yell	355	6	2.8	166	10	Q9AK31	Q9ak31 arabidopsis
283	135	15	Q9PWX9	Q9pwx9 human immun	356	6	2.8	166	16	Q9JXX9	Q9jxx9 neisseria m
284	135	15	Q9QMF6	Q9qmf6 human immun	357	6	2.8	166	16	Q9JVZ1	Q9jvz1 neisseria m
285	136	4	Q9UGZ2	Q9ugz2 homo sapien	358	6	2.8	167	15	Q9YKS7	Q9yxs7 human immun
286	136	16	Q99RY3	Q99ry3 staphylococ	359	6	2.8	168	16	Q92Y45	Q92y45 rhizobium m
287	137	15	Q94AU5	Q94au5 arabidopsis	360	6	2.8	169	2	Q9X778	Q9x778 mycobacteri
288	137	15	Q9DRS8	Q9drs8 human immun	361	6	2.8	169	12	Q917Q8	Q917q8 hepatitis c
289	138	1	Q9HH46	Q9hh46 methanobact	362	6	2.8	170	12	Q65868	Q65868 barley yell
290	138	2	Q9X3A6	Q9x3a6 unidentifie	363	6	2.8	170	17	Q980V4	Q980v4 sulfolobus
291	139	10	Q9XFE8	Q9xfe8 oryza sativ	364	6	2.8	171	5	Q9USB3	Q9usb3 caenorhabdi
292	139	15	Q9DRR3	Q9drr3 human immun	365	6	2.8	171	16	Q916L4	Q916l4 pseudomonas
293	140	11	Q79687	Q79687 human immun	366	6	2.8	172	2	Q9RGM9	Q9rgm9 neisseria g
294	140	11	Q62990	Q62990 rattus norv	367	6	2.8	172	11	Q9D7B4	Q9d7b4 mus musculu
295	140	15	Q9DHB8	Q9dhb8 human immun	368	6	2.8	173	5	Q93209	Q93209 caenorhabdi
296	140	15	Q9Q5D4	Q9q5d4 human immun	369	6	2.8	174	2	Q9AD00	Q9ad00 streptomyc
297	140	15	Q9DRR5	Q9drr5 human immun	370	6	2.8	175	2	O50239	O50239 zymomonas m
298	140	15	Q9DRR4	Q9drr4 human immun	371	6	2.8	175	4	Q9NKS5	Q9nxs5 homo sapien
299	140	15	Q9WIN0	Q9win0 human immun	372	6	2.8	176	2	Q93IK6	Q93ik6 vibrio sp.
300	140	15	Q10839	Q10839 human immun	373	6	2.8	176	15	Q74918	Q74918 human immun
301	142	2	Q9ZGX5	Q9zgx5 yersinia pe	374	6	2.8	177	2	Q9EXJ7	Q9exj7 streptomyc
302	142	12	Q66762	Q66762 encephalomy	375	6	2.8	179	10	Q9AJU5	Q9aju5 arabidopsis
303	143	2	Q93OE1	Q93qe1 streptococc	376	6	2.8	179	11	Q9CYC1	Q9cyc1 mus musculu
304	143	10	Q9FRF4	Q9frf4 oryza sativ	377	6	2.8	180	2	Q9RJM3	Q9rjm3 streptomyc
305	143	16	Q9ZNO7	Q9zn07 helicobacte	378	6	2.8	180	16	Q91766	Q91766 pseudomonas
306	144	16	O25745	O25745 helicobacte	379	6	2.8	180	16	Q92MY1	Q92my1 rhizobium m
307	144	16	Q9ZK93	Q9zk93 helicobacte	380	6	2.8	181	2	Q9XBW7	Q9xbw7 rhodobacter
308	146	12	Q9Q2Q6	Q9q2q6 human papil	381	6	2.8				

382	6	2.8	181	10	Q9XGT3	Q9xgt3 vitis vinif	455	6	2.8	200	15	Q79789	Q79789 human immun
383	6	2.8	181	15	Q9DRP1	Q9drp1 human immun	456	6	2.8	200	15	Q74842	Q74842 human immun
384	6	2.8	182	5	Q9W17	Q9w17 drosophila	457	6	2.8	200	15	Q75147	Q75147 human immun
385	6	2.8	182	15	Q80820	Q80820 human t-cel	458	6	2.8	201	15	Q9YU8	Q9yu8 human immun
386	6	2.8	182	15	Q85574	Q85574 aids-associ	459	6	2.8	201	15	Q9QRL7	Q9qrl7 human immun
387	6	2.8	182	16	Q98M88	Q98m88 rhizobium l	460	6	2.8	201	15	Q9QRL6	Q9qrl6 human immun
388	6	2.8	183	4	Q9NUS6	Q9nus6 homo sapien	461	6	2.8	201	15	Q9QRL5	Q9qrl5 human immun
389	6	2.8	183	15	Q9DRU1	Q9drul human immun	462	6	2.8	201	15	Q9QRL4	Q9qrl4 human immun
390	6	2.8	183	15	Q9KSC5	Q9ksc5 vibrio chol	463	6	2.8	201	15	Q9QRL3	Q9qrl3 human immun
391	6	2.8	184	15	Q9DRS7	Q9drs7 human immun	464	6	2.8	201	15	Q9QRL2	Q9qrl2 human immun
392	6	2.8	184	16	Q9RSY8	Q9rsy8 delnococtus	465	6	2.8	202	12	Q9Z097	Q9z097 tobacco lea
393	6	2.8	184	16	Q9RIIS6	Q9riis6 pseudomonas	466	6	2.8	202	15	Q72622	Q72622 human immun
394	6	2.8	185	2	Q9R8R4	Q9r8r4 helicobacte	467	6	2.8	202	15	Q9QPN3	Q9qpn3 human immun
395	6	2.8	185	2	Q9R8R2	Q9r8r2 helicobacte	468	6	2.8	202	15	Q91022	Q91022 human immun
396	6	2.8	185	2	Q9S229	Q9s229 streptomyce	469	6	2.8	202	15	Q75748	Q75748 human immun
397	6	2.8	185	4	Q9BX24	Q9bx24 homo sapien	470	6	2.8	202	15	P90279	P90279 human immun
398	6	2.8	185	5	Q45206	Q45206 schistosoma	471	6	2.8	202	15	P88435	P88435 human immun
399	6	2.8	185	12	Q98693	Q98693 sida golden	472	6	2.8	203	15	Q9FX46	Q9fx46 human immun
400	6	2.8	187	2	Q4805	Q4805 streptococc	473	6	2.8	203	15	Q9PX37	Q9px37 human immun
401	6	2.8	188	2	Q9L031	Q9l031 streptomyce	474	6	2.8	203	15	Q9PFW2	Q9pfw2 human immun
402	6	2.8	188	12	Q9IMV3	Q9imv3 beet wester	475	6	2.8	203	15	Q9QND7	Q9qnd7 human immun
403	6	2.8	188	15	Q9WM27	Q9wm27 human immun	476	6	2.8	203	15	Q9QND6	Q9qnd6 human immun
404	6	2.8	189	16	Q34643	Q34643 bacillus su	477	6	2.8	203	15	Q9QND5	Q9qnd5 human immun
405	6	2.8	190	12	Q9W827	Q9w827 tobacco lea	478	6	2.8	203	15	Q9QND4	Q9qnd4 human immun
406	6	2.8	190	12	Q9Z0A7	Q9z0a7 tobacco lea	479	6	2.8	203	15	Q9QND3	Q9qnd3 human immun
407	6	2.8	190	12	Q9Z095	Q9z095 tobacco lea	480	6	2.8	203	15	Q9QND2	Q9qnd2 human immun
408	6	2.8	190	12	Q9Z089	Q9z089 tobacco lea	481	6	2.8	203	15	Q9QND1	Q9qnd1 human immun
409	6	2.8	190	12	Q9Z086	Q9z086 tobacco lea	482	6	2.8	203	15	Q9QNC8	Q9qnc8 human immun
410	6	2.8	190	12	Q9Z084	Q9z084 tobacco lea	483	6	2.8	203	15	Q9QNC7	Q9qnc7 human immun
411	6	2.8	190	12	Q9Z081	Q9z081 tobacco lea	484	6	2.8	203	15	Q9QNC6	Q9qnc6 human immun
412	6	2.8	191	4	Q9HAF1	Q9haf1 homo sapien	485	6	2.8	203	15	Q9QNC5	Q9qnc5 human immun
413	6	2.8	191	10	Q94LF2	Q94lf2 oryza sativ	486	6	2.8	203	15	Q9QNC4	Q9qnc4 human immun
414	6	2.8	191	13	Q9DFC9	Q9dfc9 brachydanio	487	6	2.8	203	15	Q9QNC3	Q9qnc3 human immun
415	6	2.8	191	17	Q9HQH3	Q9hbh3 halobacteri	488	6	2.8	203	15	Q9QNC2	Q9qnc2 human immun
416	6	2.8	192	11	Q9D7J5	Q9d7j5 mus musculu	489	6	2.8	203	15	Q9QNC1	Q9qnc1 human immun
417	6	2.8	192	15	Q9WIR2	Q9wir2 human immun	490	6	2.8	203	15	Q9QNC0	Q9qnc0 human immun
418	6	2.8	192	15	Q9WIR4	Q9wir4 human immun	491	6	2.8	203	15	Q9QNC5	Q9qnc5 human immun
419	6	2.8	192	15	Q9YNB9	Q9ynb9 human immun	492	6	2.8	203	15	Q9QNC7	Q9qnc7 human immun
420	6	2.8	192	15	Q9YNB8	Q9ynb8 human immun	493	6	2.8	203	15	Q9QNC6	Q9qnc6 human immun
421	6	2.8	192	15	Q9YNE7	Q9ynb7 human immun	494	6	2.8	203	15	Q9QNC5	Q9qnc5 human immun
422	6	2.8	193	10	Q9ASF1	Q9asf1 oryza sativ	495	6	2.8	203	15	Q9IQX7	Q9iqx7 human immun
423	6	2.8	193	11	Q9ES34	Q9es34 mus musculu	496	6	2.8	203	15	Q9IQX6	Q9iqx6 human immun
424	6	2.8	194	2	Q9S406	Q9s406 proteus mir	497	6	2.8	203	15	Q9IQX5	Q9iqx5 human immun
425	6	2.8	194	15	Q9WPY0	Q9wpy0 human immun	498	6	2.8	203	15	Q9IQX4	Q9iqx4 human immun
426	6	2.8	195	4	Q9H7R4	Q9h7r4 homo sapien	499	6	2.8	203	15	Q9QMF5	Q9qmf5 human immun
427	6	2.8	196	11	Q9JKO8	Q9jkc8 mus musculu	500	6	2.8	203	15	Q9QMF4	Q9qmf4 human immun
428	6	2.8	196	13	Q9YH31	Q9yh31 notophthalm	501	6	2.8	203	15	Q9Q523	Q9q523 human immun
429	6	2.8	197	12	Q65880	Q65880 barley yell	502	6	2.8	203	15	Q9QRH3	Q9qrh3 human immun
430	6	2.8	197	15	Q10816	Q10816 human immun	503	6	2.8	203	15	Q9WPS5	Q9wps5 human immun
431	6	2.8	197	15	Q10817	Q10817 human immun	504	6	2.8	203	15	Q9JAC0	Q9jac0 human immun
432	6	2.8	197	15	Q10818	Q10818 human immun	505	6	2.8	203	15	Q9DRX1	Q9drx1 human immun
433	6	2.8	197	15	Q10820	Q10820 human immun	506	6	2.8	203	15	Q9DRX0	Q9drx0 human immun
434	6	2.8	197	15	Q10822	Q10822 human immun	507	6	2.8	203	15	Q9DRW9	Q9drw9 human immun
435	6	2.8	197	15	Q10824	Q10824 human immun	508	6	2.8	203	15	Q9DRW8	Q9drw8 human immun
436	6	2.8	197	15	Q10827	Q10827 human immun	509	6	2.8	203	15	Q9DRW7	Q9drw7 human immun
437	6	2.8	197	15	Q10828	Q10828 human immun	510	6	2.8	203	15	Q72471	Q72471 human immun
438	6	2.8	197	15	Q10829	Q10829 human immun	511	6	2.8	203	15	Q74926	Q74926 human immun
439	6	2.8	197	15	Q10829	Q10829 human immun	512	6	2.8	203	15	Q75724	Q75724 human immun
440	6	2.8	198	2	Q50927	Q50927 nitrosomona	513	6	2.8	203	15	Q75725	Q75725 human immun
441	6	2.8	198	15	Q9DRV2	Q9drv2 human immun	514	6	2.8	203	15	Q902Q5	Q902q5 human immun
442	6	2.8	198	15	Q9DRU9	Q9dru9 human immun	515	6	2.8	203	15	Q902I3	Q902i3 human immun
443	6	2.8	198	15	Q9DRU8	Q9dru8 human immun	516	6	2.8	204	12	Q901T9	Q901t9 human immun
444	6	2.8	198	15	Q9DRU7	Q9dru7 human immun	517	6	2.8	204	15	Q9Z091	Q9z091 tobacco lea
445	6	2.8	198	15	Q9DRU2	Q9drug2 human immun	518	6	2.8	204	15	Q89665	Q89665 human immun
446	6	2.8	198	15	Q74906	Q74906 human immun	519	6	2.8	204	15	Q9PXA5	Q9pxa5 human immun
447	6	2.8	198	15	Q74907	Q74907 human immun	520	6	2.8	204	15	Q9PXA5	Q9pxa5 human immun
448	6	2.8	198	15	Q74908	Q74908 human immun	521	6	2.8	204	15	Q9PX78	Q9px78 human immun
449	6	2.8	199	8	Q94R62	Q94r62 vipera beru	522	6	2.8	204	15	Q9PX09	Q9px09 human immun
450	6	2.8	199	15	Q9DRV1	Q9drv1 human immun	523	6	2.8	204	15	Q9ICH2	Q9ich2 human immun
451	6	2.8	199	15	Q76351	Q76351 human immun	524	6	2.8	204	15	Q9DGX7	Q9dgx7 human immun
452	6	2.8	200	2	Q9AD73	Q9ad73 streptomyce	525	6	2.8	204	15	Q73570	Q73570 human immun
453	6	2.8	200	2	Q93F35	Q93f35 shigella fl	526	6	2.8	204	15	Q91R12	Q91r12 human immun
454	6	2.8	200	15	Q90071	Q90071 human immun	527	6	2.8	204	15	Q91R11	Q91r11 human immun
												Q92803	Q92803 human immun

528	6	2.8	204	15	071125	071125 human immun	601	6	2.8	205	15	09WPV6	09WPV6 human immun
529	6	2.8	204	15	071127	071127 human immun	602	6	2.8	205	15	09WPV2	09WPV2 human immun
530	6	2.8	204	15	09QRH7	09qrh7 human immun	603	6	2.8	205	15	09WPV4	09WPV4 human immun
531	6	2.8	204	15	09QRH6	09qrh6 human immun	604	6	2.8	205	15	09WPT9	09wpt9 human immun
532	6	2.8	204	15	09QRH5	09qrh5 human immun	605	6	2.8	205	15	09Q096	09q096 chimpanzee
533	6	2.8	204	15	09QRH4	09qrh4 human immun	606	6	2.8	205	15	09Q098	09q098 human immun
534	6	2.8	204	15	09QRG0	09qrg0 human immun	607	6	2.8	205	15	09Q056	09q056 human immun
535	6	2.8	204	15	09QRF9	09qrf9 human immun	608	6	2.8	205	15	09Q052	09q052 human immun
536	6	2.8	204	15	09QRF8	09qrf8 human immun	609	6	2.8	205	15	09Q054	09q054 human immun
537	6	2.8	204	15	09QRF7	09qrf7 human immun	610	6	2.8	205	15	09Q050	09q050 human immun
538	6	2.8	204	15	09QRF6	09qrf6 human immun	611	6	2.8	205	15	09Q050	09q050 human immun
539	6	2.8	204	15	09WPU2	09wpu2 human immun	612	6	2.8	205	15	09Q050	09q050 human immun
540	6	2.8	204	15	09WPT4	09wpt4 human immun	613	6	2.8	205	15	09Q050	09q050 human immun
541	6	2.8	204	15	09WPT18	09wpt18 human immun	614	6	2.8	205	15	09Q050	09q050 human immun
542	6	2.8	204	15	09Q5A6	09q5a6 human immun	615	6	2.8	205	15	09Q050	09q050 human immun
543	6	2.8	204	15	09Q0Q4	09dqg4 human immun	616	6	2.8	205	15	09Q050	09q050 human immun
544	6	2.8	204	15	091031	091031 human immun	617	6	2.8	205	15	09Q050	09q050 human immun
545	6	2.8	204	15	091066	091066 human immun	618	6	2.8	205	15	09Q050	09q050 human immun
546	6	2.8	204	15	092473	092473 human immun	619	6	2.8	205	15	09Q050	09q050 human immun
547	6	2.8	204	15	099842	099842 human immun	620	6	2.8	205	15	09Q050	09q050 human immun
548	6	2.8	204	15	074919	074919 human immun	621	6	2.8	205	15	09Q050	09q050 human immun
549	6	2.8	204	15	074920	074920 human immun	622	6	2.8	205	15	09Q050	09q050 human immun
550	6	2.8	204	15	074921	074921 human immun	623	6	2.8	205	15	09Q050	09q050 human immun
551	6	2.8	204	15	075621	075621 human immun	624	6	2.8	205	15	09Q050	09q050 human immun
552	6	2.8	204	15	075622	075622 human immun	625	6	2.8	205	15	09Q050	09q050 human immun
553	6	2.8	204	15	075631	075631 human immun	626	6	2.8	205	15	09Q050	09q050 human immun
554	6	2.8	204	15	075632	075632 human immun	627	6	2.8	205	15	09Q050	09q050 human immun
555	6	2.8	204	15	075143	075143 human immun	628	6	2.8	205	15	09Q050	09q050 human immun
556	6	2.8	204	15	075144	075144 human immun	629	6	2.8	205	15	09Q050	09q050 human immun
557	6	2.8	204	15	090266	090266 human immun	630	6	2.8	205	15	09Q050	09q050 human immun
558	6	2.8	204	15	075751	075751 human immun	631	6	2.8	205	15	09Q050	09q050 human immun
559	6	2.8	204	15	076352	076352 human immun	632	6	2.8	205	15	09Q050	09q050 human immun
560	6	2.8	204	15	07YNC0	07ync0 human immun	633	6	2.8	205	15	09Q050	09q050 human immun
561	6	2.8	204	15	040601	040601 human immun	634	6	2.8	205	15	09Q050	09q050 human immun
562	6	2.8	204	15	0902H4	0902h4 human immun	635	6	2.8	205	15	09Q050	09q050 human immun
563	6	2.8	205	2	Q9S2M0	Q9s2m0 streptomyce	636	6	2.8	205	15	09Q050	09q050 human immun
564	6	2.8	205	15	Q89586	Q89586 human immun	637	6	2.8	205	15	09Q050	09q050 human immun
565	6	2.8	205	15	Q89623	Q89623 human immun	638	6	2.8	205	15	09Q050	09q050 human immun
566	6	2.8	205	15	072436	072436 human immun	639	6	2.8	205	15	09Q050	09q050 human immun
567	6	2.8	205	15	075713	075713 human immun	640	6	2.8	205	15	09Q050	09q050 human immun
568	6	2.8	205	15	Q9W805	Q9w805 human immun	641	6	2.8	205	15	09Q050	09q050 human immun
569	6	2.8	205	15	Q9PX72	Q9px72 human immun	642	6	2.8	205	15	09Q050	09q050 human immun
570	6	2.8	205	15	Q9PX02	Q9px02 human immun	643	6	2.8	205	15	09Q050	09q050 human immun
571	6	2.8	205	15	Q9PX00	Q9px00 human immun	644	6	2.8	205	15	09Q050	09q050 human immun
572	6	2.8	205	15	Q9PWZ8	Q9pwz8 human immun	645	6	2.8	205	15	09Q050	09q050 human immun
573	6	2.8	205	15	040592	040592 human immun	646	6	2.8	205	15	09Q050	09q050 human immun
574	6	2.8	205	15	Q9DGU1	Q9dgu1 human immun	647	6	2.8	205	15	09Q050	09q050 human immun
575	6	2.8	205	15	Q9QNF1	Q9qnf1 human immun	648	6	2.8	205	15	09Q050	09q050 human immun
576	6	2.8	205	15	Q9QNF0	Q9qnf0 human immun	649	6	2.8	205	15	09Q050	09q050 human immun
577	6	2.8	205	15	Q9QNE9	Q9qne9 human immun	650	6	2.8	205	15	09Q050	09q050 human immun
578	6	2.8	205	15	Q9QNE8	Q9qne8 human immun	651	6	2.8	205	15	09Q050	09q050 human immun
579	6	2.8	205	15	Q9QNE6	Q9qne6 human immun	652	6	2.8	205	15	09Q050	09q050 human immun
580	6	2.8	205	15	Q9QNE5	Q9qne5 human immun	653	6	2.8	205	15	09Q050	09q050 human immun
581	6	2.8	205	15	Q9QNE3	Q9qne3 human immun	654	6	2.8	205	15	09Q050	09q050 human immun
582	6	2.8	205	15	Q9QND8	Q9qnd8 human immun	655	6	2.8	205	15	09Q050	09q050 human immun
583	6	2.8	205	15	Q9WLX6	Q9w1x6 human immun	656	6	2.8	205	15	09Q050	09q050 human immun
584	6	2.8	205	15	Q9WLX5	Q9w1x5 human immun	657	6	2.8	205	15	09Q050	09q050 human immun
585	6	2.8	205	15	071126	071126 human immun	658	6	2.8	205	15	09Q050	09q050 human immun
586	6	2.8	205	15	09YX71	09yx71 human immun	659	6	2.8	205	15	09Q050	09q050 human immun
587	6	2.8	205	15	072628	072628 human immun	660	6	2.8	205	15	09Q050	09q050 human immun
588	6	2.8	205	15	072631	072631 human immun	661	6	2.8	205	15	09Q050	09q050 human immun
589	6	2.8	205	15	Q9QSO6	Q9qsg6 human immun	662	6	2.8	205	15	09Q050	09q050 human immun
590	6	2.8	205	15	09Q500	09Q500 human immun	663	6	2.8	205	15	09Q050	09q050 human immun
591	6	2.8	205	15	090509	090509 human immun	664	6	2.8	205	15	09Q050	09q050 human immun
592	6	2.8	205	15	090521	090521 human immun	665	6	2.8	205	15	09Q050	09q050 human immun
593	6	2.8	205	15	090522	090522 human immun	666	6	2.8	205	15	09Q050	09q050 human immun
594	6	2.8	205	15	090528	090528 human immun	667	6	2.8	205	15	09Q050	09q050 human immun
595	6	2.8	205	15	090645	090645 human immun	668	6	2.8	205	15	09Q050	09q050 human immun
596	6	2.8	205	15	09QRJ0	09qrj0 human immun	669	6	2.8	205	15	09Q050	09q050 human immun
597	6	2.8	205	15	09QRE7	09qre7 human immun	670	6	2.8	205	15	09Q050	09q050 human immun
598	6	2.8	205	15	Q9WPX8	Q9wp8 human immun	671	6	2.8	205	15	09Q050	09q050 human immun
599	6	2.8	205	15	Q9WPW2	Q9wpw2 human immun	672	6	2.8	205	15	09Q050	09q050 human immun
600	6	2.8	205	15	Q9WPV9	Q9wpv9 human immun	673	6	2.8	205	15	09Q050	09q050 human immun

674	6	2.8	205	15	Q75714	Q75714 human	747	6	2.8	206	15	Q9PWW0	Q9PWW0 human
675	6	2.8	205	15	Q75715	Q75715 human	748	6	2.8	206	15	Q9PWT7	Q9PWT7 human
676	6	2.8	205	15	Q75716	Q75716 human	749	6	2.8	206	15	Q9WA35	Q9WA35 human
677	6	2.8	205	15	Q75717	Q75717 human	750	6	2.8	206	15	Q9IR09	Q9IR09 human
678	6	2.8	205	15	Q88405	Q88405 human	751	6	2.8	206	15	Q9IR08	Q9IR08 human
679	6	2.8	205	15	Q88407	Q88407 human	752	6	2.8	206	15	Q9IR07	Q9IR07 human
680	6	2.8	205	15	Q88408	Q88408 human	753	6	2.8	206	15	Q9IR06	Q9IR06 human
681	6	2.8	205	15	Q88409	Q88409 human	754	6	2.8	206	15	Q9IR05	Q9IR05 human
682	6	2.8	205	15	Q88410	Q88410 human	755	6	2.8	206	15	Q9IQ29	Q9IQ29 human
683	6	2.8	205	15	Q88411	Q88411 human	756	6	2.8	206	15	Q9IQ28	Q9IQ28 human
684	6	2.8	205	15	Q88412	Q88412 human	757	6	2.8	206	15	Q9IQ26	Q9IQ26 human
685	6	2.8	205	15	Q88413	Q88413 human	758	6	2.8	206	15	Q9IQ25	Q9IQ25 human
686	6	2.8	205	15	Q88414	Q88414 human	759	6	2.8	206	15	Q9IQ24	Q9IQ24 human
687	6	2.8	205	15	Q88415	Q88415 human	760	6	2.8	206	15	Q9IQ23	Q9IQ23 human
688	6	2.8	205	15	Q88416	Q88416 human	761	6	2.8	206	15	Q9IQ21	Q9IQ21 human
689	6	2.8	205	15	Q88417	Q88417 human	762	6	2.8	206	15	Q40177	Q40177 human
690	6	2.8	205	15	Q88418	Q88418 human	763	6	2.8	206	15	Q40178	Q40178 human
691	6	2.8	205	15	Q88420	Q88420 human	764	6	2.8	206	15	Q40223	Q40223 human
692	6	2.8	205	15	Q88421	Q88421 human	765	6	2.8	206	15	Q70896	Q70896 human
693	6	2.8	205	15	Q88422	Q88422 human	766	6	2.8	206	15	Q9WM29	Q9WM29 human
694	6	2.8	205	15	Q88423	Q88423 human	767	6	2.8	206	15	Q9WM28	Q9WM28 human
695	6	2.8	205	15	Q88424	Q88424 human	768	6	2.8	206	15	Q9WM24	Q9WM24 human
696	6	2.8	205	15	Q88425	Q88425 human	769	6	2.8	206	15	Q9WM23	Q9WM23 human
697	6	2.8	205	15	Q88427	Q88427 human	770	6	2.8	206	15	Q9WM17	Q9WM17 human
698	6	2.8	205	15	Q88428	Q88428 human	771	6	2.8	206	15	Q9WM16	Q9WM16 human
699	6	2.8	205	15	Q88429	Q88429 human	772	6	2.8	206	15	Q92771	Q92771 human
700	6	2.8	205	15	Q88430	Q88430 human	773	6	2.8	206	15	Q9WIX9	Q9WIX9 human
701	6	2.8	205	15	Q76349	Q76349 human	774	6	2.8	206	15	Q9WIX8	Q9WIX8 human
702	6	2.8	205	15	Q76350	Q76350 human	775	6	2.8	206	15	Q71085	Q71085 human
703	6	2.8	205	15	Q40591	Q40591 human	776	6	2.8	206	15	Q9WIX7	Q9WIX7 human
704	6	2.8	205	15	Q90MK4	Q90MK4 human	777	6	2.8	206	15	Q71086	Q71086 human
705	6	2.8	205	15	Q908M1	Q908M1 human	778	6	2.8	206	15	Q9WIX4	Q9WIX4 human
706	6	2.8	205	15	Q908K3	Q908K3 human	779	6	2.8	206	15	Q9WIX3	Q9WIX3 human
707	6	2.8	205	15	Q908J4	Q908J4 human	780	6	2.8	206	15	Q92772	Q92772 human
708	6	2.8	205	15	Q908I5	Q908I5 human	781	6	2.8	206	15	Q9WIX2	Q9WIX2 human
709	6	2.8	205	15	Q902U1	Q902U1 human	782	6	2.8	206	15	Q9WIX1	Q9WIX1 human
710	6	2.8	205	15	Q902S3	Q902S3 human	783	6	2.8	206	15	Q9WIX0	Q9WIX0 human
711	6	2.8	205	15	Q902P6	Q902P6 human	784	6	2.8	206	15	Q71087	Q71087 human
712	6	2.8	205	15	Q902N7	Q902N7 human	785	6	2.8	206	15	Q9WIX9	Q9WIX9 human
713	6	2.8	205	15	Q902G5	Q902G5 human	786	6	2.8	206	15	Q92887	Q92887 human
714	6	2.8	206	12	Q92094	Q92094 tobacco	787	6	2.8	206	15	Q9WIM7	Q9WIM7 human
715	6	2.8	206	13	Q9YGD8	Q9YGD8 oncorhynch	788	6	2.8	206	15	Q9WIM6	Q9WIM6 human
716	6	2.8	206	15	Q9S561	Q9S561 human	789	6	2.8	206	15	Q9WIM5	Q9WIM5 human
717	6	2.8	206	15	Q99766	Q99766 human	790	6	2.8	206	15	Q9WIM4	Q9WIM4 human
718	6	2.8	206	15	Q99896	Q99896 human	791	6	2.8	206	15	Q92938	Q92938 human
719	6	2.8	206	15	Q99553	Q99553 human	792	6	2.8	206	15	Q9WIL6	Q9WIL6 human
720	6	2.8	206	15	Q99880	Q99880 human	793	6	2.8	206	15	Q72621	Q72621 human
721	6	2.8	206	15	Q99430	Q99430 human	794	6	2.8	206	15	Q72623	Q72623 human
722	6	2.8	206	15	Q99436	Q99436 human	795	6	2.8	206	15	Q72625	Q72625 human
723	6	2.8	206	15	Q99511	Q99511 human	796	6	2.8	206	15	Q72626	Q72626 human
724	6	2.8	206	15	Q99515	Q99515 human	797	6	2.8	206	15	Q72629	Q72629 human
725	6	2.8	206	15	Q99537	Q99537 human	798	6	2.8	206	15	Q93010	Q93010 human
726	6	2.8	206	15	Q99575	Q99575 human	799	6	2.8	206	15	Q72632	Q72632 human
727	6	2.8	206	15	Q99587	Q99587 human	800	6	2.8	206	15	Q72635	Q72635 human
728	6	2.8	206	15	Q99630	Q99630 human	801	6	2.8	206	15	Q72636	Q72636 human
729	6	2.8	206	15	Q99668	Q99668 human	802	6	2.8	206	15	Q72647	Q72647 human
730	6	2.8	206	15	Q99688	Q99688 human	803	6	2.8	206	15	Q72648	Q72648 human
731	6	2.8	206	15	Q99706	Q99706 human	804	6	2.8	206	15	Q72649	Q72649 human
732	6	2.8	206	15	Q99778	Q99778 human	805	6	2.8	206	15	Q72650	Q72650 human
733	6	2.8	206	15	Q99851	Q99851 human	806	6	2.8	206	15	Q72651	Q72651 human
734	6	2.8	206	15	Q99888	Q99888 human	807	6	2.8	206	15	Q72652	Q72652 human
735	6	2.8	206	15	Q99889	Q99889 human	808	6	2.8	206	15	Q93012	Q93012 human
736	6	2.8	206	15	Q12390	Q12390 human	809	6	2.8	206	15	Q9W7X3	Q9W7X3 human
737	6	2.8	206	15	Q12404	Q12404 human	810	6	2.8	206	15	Q9W7X2	Q9W7X2 human
738	6	2.8	206	15	Q99629	Q99629 human	811	6	2.8	206	15	Q93013	Q93013 human
739	6	2.8	206	15	Q9YJ66	Q9YJ66 human	812	6	2.8	206	15	Q93014	Q93014 human
740	6	2.8	206	15	Q75752	Q75752 human	813	6	2.8	206	15	Q9W7X1	Q9W7X1 human
741	6	2.8	206	15	Q75718	Q75718 human	814	6	2.8	206	15	Q9W7X0	Q9W7X0 human
742	6	2.8	206	15	Q9W9N0	Q9W9N0 human	815	6	2.8	206	15	Q90179	Q90179 human
743	6	2.8	206	15	Q9W7U0	Q9W7U0 human	816	6	2.8	206	15	Q9QSU1	Q9QSU1 human
744	6	2.8	206	15	Q9PWX9	Q9PWX9 human	817	6	2.8	206	15	Q90502	Q90502 human
745	6	2.8	206	15	Q9PWX8	Q9PWX8 human	818	6	2.8	206	15	Q90505	Q90505 human
746	6	2.8	206	15	Q9PXX7	Q9PXX7 human	819	6	2.8	206	15	Q90511	Q90511 human

820	6	2.8	206	15	090526	090526 human immun	893	6	2.8	206	15	0905E5	0905E5 human immun
821	6	2.8	206	15	090644	090644 human immun	894	6	2.8	206	15	0905D6	0905D6 human immun
822	6	2.8	206	15	090RX0	090RX0 human immun	895	6	2.8	206	15	0905D5	0905D5 human immun
823	6	2.8	206	15	090RL1	090RL1 human immun	896	6	2.8	206	15	0905D3	0905D3 human immun
824	6	2.8	206	15	090RL0	090RL0 human immun	897	6	2.8	206	15	0905D2	0905D2 human immun
825	6	2.8	206	15	090RK9	090RK9 human immun	898	6	2.8	206	15	0905B9	0905B9 human immun
826	6	2.8	206	15	090RK8	090RK8 human immun	899	6	2.8	206	15	0905B8	0905B8 human immun
827	6	2.8	206	15	090RK7	090RK7 human immun	900	6	2.8	206	15	0905B1	0905B1 human immun
828	6	2.8	206	15	090RK6	090RK6 human immun	901	6	2.8	206	15	0905B0	0905B0 human immun
829	6	2.8	206	15	090RK5	090RK5 human immun	902	6	2.8	206	15	0905A8	0905A8 human immun
830	6	2.8	206	15	090RK4	090RK4 human immun	903	6	2.8	206	15	0905A7	0905A7 human immun
831	6	2.8	206	15	090RK3	090RK3 human immun	904	6	2.8	206	15	0905A3	0905A3 human immun
832	6	2.8	206	15	090RK2	090RK2 human immun	905	6	2.8	206	15	090599	090599 human immun
833	6	2.8	206	15	090RK1	090RK1 human immun	906	6	2.8	206	15	090598	090598 human immun
834	6	2.8	206	15	090RJ2	090RJ2 human immun	907	6	2.8	206	15	090597	090597 human immun
835	6	2.8	206	15	090RJ1	090RJ1 human immun	908	6	2.8	206	15	090596	090596 human immun
836	6	2.8	206	15	090RT3	090RT3 human immun	909	6	2.8	206	15	090595	090595 human immun
837	6	2.8	206	15	090RT2	090RT2 human immun	910	6	2.8	206	15	090594	090594 human immun
838	6	2.8	206	15	090RT1	090RT1 human immun	911	6	2.8	206	15	090DR3	090DR3 human immun
839	6	2.8	206	15	090RI0	090RI0 human immun	912	6	2.8	206	15	090DR2	090DR2 human immun
840	6	2.8	206	15	090RH9	090RH9 human immun	913	6	2.8	206	15	090DR1	090DR1 human immun
841	6	2.8	206	15	090RH8	090RH8 human immun	914	6	2.8	206	15	090DR0	090DR0 human immun
842	6	2.8	206	15	090RF5	090RF5 human immun	915	6	2.8	206	15	090DRV9	090DRV9 human immun
843	6	2.8	206	15	090RF4	090RF4 human immun	916	6	2.8	206	15	090DRV8	090DRV8 human immun
844	6	2.8	206	15	090RF3	090RF3 human immun	917	6	2.8	206	15	090DRV7	090DRV7 human immun
845	6	2.8	206	15	090RF2	090RF2 human immun	918	6	2.8	206	15	090DRV6	090DRV6 human immun
846	6	2.8	206	15	090RF1	090RF1 human immun	919	6	2.8	206	15	090DRV5	090DRV5 human immun
847	6	2.8	206	15	090PY2	090PY2 human immun	920	6	2.8	206	15	090DRV4	090DRV4 human immun
848	6	2.8	206	15	090PY1	090PY1 human immun	921	6	2.8	206	15	090DR06	090DR06 human immun
849	6	2.8	206	15	090PX7	090PX7 human immun	922	6	2.8	206	15	090DR05	090DR05 human immun
850	6	2.8	206	15	090PX3	090PX3 human immun	923	6	2.8	206	15	090DR02	090DR02 human immun
851	6	2.8	206	15	090PX2	090PX2 human immun	924	6	2.8	206	15	090DRS9	090DRS9 human immun
852	6	2.8	206	15	090PX0	090PX0 human immun	925	6	2.8	206	15	090DRS4	090DRS4 human immun
853	6	2.8	206	15	090PW9	090PW9 human immun	926	6	2.8	206	15	090DRS3	090DRS3 human immun
854	6	2.8	206	15	090PW6	090PW6 human immun	927	6	2.8	206	15	090DRS2	090DRS2 human immun
855	6	2.8	206	15	090PW4	090PW4 human immun	928	6	2.8	206	15	090DRS1	090DRS1 human immun
856	6	2.8	206	15	090PW0	090PW0 human immun	929	6	2.8	206	15	090DRR9	090DRR9 human immun
857	6	2.8	206	15	090PV8	090PV8 human immun	930	6	2.8	206	15	090J0G4	090J0G4 human immun
858	6	2.8	206	15	090PV7	090PV7 human immun	931	6	2.8	206	15	091H71	091H71 human immun
859	6	2.8	206	15	090PV4	090PV4 human immun	932	6	2.8	206	15	091H69	091H69 human immun
860	6	2.8	206	15	090PV3	090PV3 human immun	933	6	2.8	206	15	091H68	091H68 human immun
861	6	2.8	206	15	090PV2	090PV2 human immun	934	6	2.8	206	15	091H67	091H67 human immun
862	6	2.8	206	15	090PV1	090PV1 human immun	935	6	2.8	206	15	091H65	091H65 human immun
863	6	2.8	206	15	090PW6	090PW6 human immun	936	6	2.8	206	15	091H64	091H64 human immun
864	6	2.8	206	15	090PW0	090PW0 human immun	937	6	2.8	206	15	090DQ1	090DQ1 human immun
865	6	2.8	206	15	090PV8	090PV8 human immun	938	6	2.8	206	15	090DQ19	090DQ19 human immun
866	6	2.8	206	15	090PV7	090PV7 human immun	939	6	2.8	206	15	090DQ16	090DQ16 human immun
867	6	2.8	206	15	090PV4	090PV4 human immun	940	6	2.8	206	15	090DQ15	090DQ15 human immun
868	6	2.8	206	15	090PV3	090PV3 human immun	941	6	2.8	206	15	090DQ13	090DQ13 human immun
869	6	2.8	206	15	090PV2	090PV2 human immun	942	6	2.8	206	15	090DQ12	090DQ12 human immun
870	6	2.8	206	15	090PV1	090PV1 human immun	943	6	2.8	206	15	090DQ11	090DQ11 human immun
871	6	2.8	206	15	090PW0	090PW0 human immun	944	6	2.8	206	15	090DQ00	090DQ00 human immun
872	6	2.8	206	15	090PW5	090PW5 human immun	945	6	2.8	206	15	090DQF8	090DQF8 human immun
873	6	2.8	206	15	090PW9	090PW9 human immun	946	6	2.8	206	15	090DQF7	090DQF7 human immun
874	6	2.8	206	15	090WP17	090WP17 human immun	947	6	2.8	206	15	090DQF6	090DQF6 human immun
875	6	2.8	206	15	090WP16	090WP16 human immun	948	6	2.8	206	15	090DQF5	090DQF5 human immun
876	6	2.8	206	15	090WP14	090WP14 human immun	949	6	2.8	206	15	090DQF4	090DQF4 human immun
877	6	2.8	206	15	090WP11	090WP11 human immun	950	6	2.8	206	15	090DQF3	090DQF3 human immun
878	6	2.8	206	15	090WF2	090WF2 human immun	951	6	2.8	206	15	090E2H7	090E2H7 human immun
879	6	2.8	206	15	090Q080	090Q080 chimpanzee	952	6	2.8	206	15	0994Q05	0994Q05 human immun
880	6	2.8	206	15	090Q6W8	090Q6W8 human immun	953	6	2.8	206	15	0994N7	0994N7 human immun
881	6	2.8	206	15	090Q5H6	090Q5H6 human immun	954	6	2.8	206	15	0994L0	0994L0 human immun
882	6	2.8	206	15	090Q5H5	090Q5H5 human immun	955	6	2.8	206	15	0994K1	0994K1 human immun
883	6	2.8	206	15	090Q5H4	090Q5H4 human immun	956	6	2.8	206	15	0994F6	0994F6 human immun
884	6	2.8	206	15	090Q5H3	090Q5H3 human immun	957	6	2.8	206	15	093025	093025 human immun
885	6	2.8	206	15	090Q5F8	090Q5F8 human immun	958	6	2.8	206	15	091010	091010 human immun
886	6	2.8	206	15	090Q5F7	090Q5F7 human immun	959	6	2.8	206	15	091025	091025 human immun
887	6	2.8	206	15	090Q5F2	090Q5F2 human immun	960	6	2.8	206	15	091053	091053 human immun
888	6	2.8	206	15	090Q5F1	090Q5F1 human immun	961	6	2.8	206	15	09WK41	09WK41 human immun
889	6	2.8	206	15	090Q5F0	090Q5F0 human immun	962	6	2.8	206	15	09WK40	09WK40 human immun
890	6	2.8	206	15	090Q5E9	090Q5E9 human immun	963	6	2.8	206	15	091034	091034 human immun
891	6	2.8	206	15	090Q5E8	090Q5E8 human immun	964	6	2.8	206	15	091035	091035 human immun
892	6	2.8	206	15	090Q5E7	090Q5E7 human immun	965	6	2.8	206	15	091056	091056 human immun

966 6 2.8 206 15 O91059 human immun
967 6 2.8 206 15 O91061 human immun
968 6 2.8 206 15 O9WK39 human immun
969 6 2.8 206 15 O91062 human immun
970 6 2.8 206 15 O9WK38 human immun
971 6 2.8 206 15 O91072 human immun
972 6 2.8 206 15 O91073 human immun
973 6 2.8 206 15 O91074 human immun
974 6 2.8 206 15 O91075 human immun
975 6 2.8 206 15 O9DKF7 human immun
976 6 2.8 206 15 O9DKF9 human immun
977 6 2.8 206 15 O9DKF1 human immun
978 6 2.8 206 15 O97883 human immun
979 6 2.8 206 15 O97882 human immun
980 6 2.8 206 15 O97673 human immun
981 6 2.8 206 15 O97674 human immun
982 6 2.8 206 15 O97675 human immun
983 6 2.8 206 15 O97676 human immun
984 6 2.8 206 15 O97677 human immun
985 6 2.8 206 15 O97678 human immun
986 6 2.8 206 15 O97680 human immun
987 6 2.8 206 15 O97681 human immun
988 6 2.8 206 15 O97683 human immun
989 6 2.8 206 15 O97684 human immun
990 6 2.8 206 15 O97685 human immun
991 6 2.8 206 15 O97688 human immun
992 6 2.8 206 15 O97689 human immun
993 6 2.8 206 15 O97690 human immun
994 6 2.8 206 15 O97691 human immun
995 6 2.8 206 15 O97692 human immun
996 6 2.8 206 15 O97693 human immun
997 6 2.8 206 15 O97694 human immun
998 6 2.8 206 15 O97695 human immun
999 6 2.8 206 15 O97696 human immun
1000 6 2.8 206 15 O97697 human immun

ALIGNMENTS

RESULT 1
Q9EST9 ID Q9EST9 PRELIMINARY; PRT; 212 AA.
AC Q9EST9; 2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FGF-20.
GN FGF-20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=ADULT BRAIN;
MEDLINE=20490008; PubMed=11032730;
RA Ohmachi S., Watanabe Y., Mikami T., Kusu N., Ibi T., Akaike A.,
Itoh N.;
RA "FGF-20, a novel neurotrophic factor, preferentially expressed in the
RT substantia nigra pars compacta of rat brain."
RL Biochem. Biophys. Res. Commun. 277:355-360(2000).
DR EMBL; AB020021; BAB13763.1; -;
DR HSSP; P31371; IG82.
DR InterPro; IPR002209; HBGFG_FGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; HBGFG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 212 AA; 29537 MW; 4F858BEFE772B977 CRC64;

Query Match 40.3%; Score 85; DB 11; Length 212;
Best Local Similarity 100.0%; Pred. No. 9.2e-79;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 KGELYGSEKLTSECIFRQEEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKR 183
DB 124 KGELYGSEKLTSECIFRQEEENWYNTYSSNIYKHGDTGRRYFVALNKDGTPRDGARSKR 183
QY 184 HOKFTFLPRVDPERPVELYKDLL 208
DB 184 HOKFTFLPRVDPERPVELYKDLL 208
RESULT 2
Q9ESL9 ID Q9ESL9 PRELIMINARY; PRT; 212 AA.
AC Q9ESL9; 2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 20.
GN FGF20.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itoh N.;
RT "Mus musculus mRNA for FGF-20(FGF20).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049218; BAB16406.1; -;
DR HSSP; P31371; IG82.
DR MGD; MGI:1891346; Fgf20.
DR InterPro; IPR002209; HBGFG_FGF.
DR InterPro; IPR002348; IL1HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD000831; HBGFG_FGF; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 212 AA; 23659 MW; 174DBCE8915B69EF CRC64;
Query Match 35.5%; Score 75; DB 11; Length 212;
Best Local Similarity 100.0%; Pred. No. 1.6e-68;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 85 VQGTQDHSLSGLFISVAVGLSVIRGVDGLYGMNDKGLYSEKLTSECIFRQEE 144
DB 85 VQGTQDHSLSGLFISVAVGLSVIRGVDGLYGMNDKGLYSEKLTSECIFRQEE 144
QY 145 ENWYNTYSSNIYKHG 159
DB 145 ENWYNTYSSNIYKHG 159
RESULT 3
Q9PVY1 ID Q9PVY1 PRELIMINARY; PRT; 208 AA.
AC Q9PVY1; 2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE XFGF-20.
GN XFGF-20.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99373151; PubMed=10441498;


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RA Koga C., Adati N., Nakata K., Mikoshiba K., Furuhata Y., Sato S.,
RA Tei H., Sakaki Y., Kurokawa T., Shiohara K., Yokoyama K.K.:
RT "Characterization of a novel member of the FGF family, XFGF-20, in
RL Xenopus laevis."; Res. Commun. 261:756-765(1999).
DR Biochem. Biophys. 261:756-765(1999).
DR EMBL: AB012615; BAA83474.1; -.
DR HSSP: P31371; IG82.
DR InterPro: IPR002209; HBGFG_FGF.
DR InterPro: IPR002348; ILI_HBGFG.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; ILI_HBGFG.
DR ProDom: PD000831; HBGFG_FGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 208 AA; 23438 MW; 268881D36E757D4D CRC64;

Query Match 12.3%; Score 26; DB 13; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 GSEKLTSECFRQFEENWYSSN 154
DB 126 GSEKLTSECFRQFEENWYSSN 151
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RESULT 4
ID Q95L12 PRELIMINARY; PRT; 208 AA.
AC Q95L12;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 9.
GN FGF9.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP PARADIS V., Silversides D.W.;
RA "Sus scrofa fgf9 cDNA.";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY033825; AAK61609.2; -.
SQ SEQUENCE 208 AA; 23454 MW; 05FD0E2048CCC5E5 CRC64;

Query Match 9.0%; Score 19; DB 6; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 104 AVGLVSRGVDSGLYLGMN 122
DB 101 AVGLVSRGVDSGLYLGMN 119
|||||
RESULT 5
ID Q9ESL8 PRELIMINARY; PRT; 207 AA.
AC Q9ESL8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FIBROBLAST GROWTH FACTOR 16.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Itch N.;
RT "Mus musculus mRNA for FGF-16 (FGF16).";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AB049219; BAB16405.1; -.
DR HSSP: P31371; IG82.
DR MGD: MGI:1931627; Fgf16.
DR InterPro: IPR002209; HBGFG_FGF.
DR InterPro: IPR002348; ILI_HBGFG.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; ILI_HBGFG.
DR ProDom: PD000831; HBGFG_FGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 207 AA; 23751 MW; 68BD03EBDAAD1D84E CRC64;

Query Match 7.6%; Score 16; DB 11; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLYCRGTGFHL 77
DB 58 GILRRRLYCRGTGFHL 73
|||||
RESULT 6
ID Q9ERQ5 PRELIMINARY; PRT; 207 AA.
AC Q9ERQ5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FGF-16 PROTEIN.
GN FGF16.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Sontag D.P., Cattini P.A.;
RT "Cloning and biological function of FGF-16 in the heart.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF292104; AAG29501.1; -.
DR HSSP: P31371; IG82.
DR MGD: MGI:1931627; Fgf16.
DR InterPro: IPR002209; HBGFG_FGF.
DR InterPro: IPR002348; ILI_HBGFG.
DR Pfam: PF00167; FGF; 1.
DR PRINTS: PR00262; ILI_HBGFG.
DR ProDom: PD000831; HBGFG_FGF; 1.
DR SMART: SM00442; FGF; 1.
DR PROSITE: PS00247; HBGFG_FGF; 1.
SQ SEQUENCE 207 AA; 23739 MW; E28004DED598A2C6 CRC64;

Query Match 7.6%; Score 16; DB 11; Length 207;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 62 GILRRRLYCRGTGFHL 77
DB 58 GILRRRLYCRGTGFHL 73
|||||
RESULT 7
ID Q9S9P9 PRELIMINARY; PRT; 197 AA.
AC Q9S9P9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F26G16.12 PROTEIN.
GN F26G16.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S.X., Sakano H., Yu G., Jhaveri A., Lee J.M., Lenz C., Pham P.,
RA Toriumi M., Chin C., Chlou J., Choi E., Chung M., Gonzalez A.,
RA Hwang B., Koo T., Li J., Liu A., Vaysberg M., Altafi H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A., Hansen N., Johnson-Hopson C.,
RA Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC F26G16 sequence.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009917; AAF19754.1; -.
DR InterPro; IPR001289; CBF_NFYA.
DR Pfam; PF02045; CBF_NFYA; 1.
DR PRINTS; PR00616; CCAATSUBUNT.
DR ProDom; PD003860; CBF_NFYA; 1.
DR SMART; SM00521; CBF; 1.
SQ SEQUENCE 197 AA; 22127 MW; EB67C5050BE0F874 CRC64;

Query Match 3.8%; Score 8; DB 10; Length 197;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
DB 117 HGILRRRQ 124

RESULT 8
Q9M607 PRELIMINARY; PRT; 215 AA.
ID Q9M607
AC Q9M607
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE TRANSCRIPTION FACTOR.
GN REV136-2.
OS Vitis riparia (Frost grape) (Vitis vulpina).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
OC Vitis.
OX NCBI_TaxID=96939;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FLOWER BUDS;
RA Li X.Z., McKersie B.D.;
RT "Freezing tolerance in grapevines.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF220405; AAF37266.1; -.
DR InterPro; IPR001289; CBF_NFYA.
DR Pfam; PF02045; CBF_NFYA; 1.
DR PRINTS; PR00616; CCAATSUBUNT.
DR ProDom; PD003860; CBF_NFYA; 1.
DR SMART; SM00521; CBF; 1.
SQ SEQUENCE 215 AA; 24311 MW; EBCB7BB5921E415E CRC64;

Query Match 3.8%; Score 8; DB 10; Length 215;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
DB 56 HGILRRRQ 63

RESULT 9

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O64585 PRELIMINARY; PRT; 226 AA.
ID O64585
AC O64585
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE CCAAT-BOX-BINDING TRANSCRIPTION FACTOR SUBUNIT.
GN AT2G34720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC003096; AAC16262.1; -.
DR InterPro; IPR001289; CBF_NFYA.
DR Pfam; PF02045; CBF_NFYA; 1.
DR PRINTS; PR00616; CCAATSUBUNT.
DR ProDom; PD003860; CBF_NFYA; 1.
DR SMART; SM00521; CBF; 1.
SQ SEQUENCE 226 AA; 25786 MW; 35047340C2202018 CRC64;

Query Match 3.8%; Score 8; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 HGILRRRQ 68
DB 136 HGILRRRQ 143

RESULT 10
O70128 PRELIMINARY; PRT; 275 AA.
ID O70128
AC O70128
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PUTATIVE AIPASE (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98217376; PubMed=9548971;
RA Halleck M.S., Pradhan D., Blackman C., Berkes C., Williamson P.,
RA Schlegel R.A.;
RT "Multiple members of a third subfamily of P-type ATPases identified by
genomic sequences and ESTs.";
RL Genome Res. 8:354-361(1998).
DR EMBL; U78977; AAC05244.1; -.
DR InterPro; IPR000150; Hypothet_cof.
DR NON_TER 1
FT SEQUENCE 275 AA; 31000 MW; 067CF9B1F80A5879 CRC64;

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Query Match 3.8%; Score 8; DB 11; Length 275;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PELYKDLL 208
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Db 135 PELYKDLL 142

RESULT 11
Q9M332 ID Q9M332 PRELIMINARY; PRT; 545 AA.
AC Q9M332;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 60.0 KDA PROTEIN (AT3G53950/F5K20_250).
GN F5K20_250.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Monfort A., Casacuberta E., Puigdomenech P., Mewes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quetier E., Salanoubat M.;
RA Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RA "Arabidopsis cDNA clones."
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AL132960; CAB88357.1; -.
DR EMBL: AY054205; AAL08666.1; -.
KW Hypothetical protein.
SQ SEQUENCE 545 AA; 60004 MW; 14745A770BBB53C5 CRC64;

Query Match 3.8%; Score 8; DB 10; Length 545;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 QILPDGSV 85
    |||||
Db 172 QILPDGSV 179

RESULT 12
Q9X2Y5 ID Q9X2Y5 PRELIMINARY; PRT; 564 AA.
AC Q9X2Y5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PX01-14.
OS Bacillus anthracis.
OG Plasmid virulence plasmid pX01.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1392;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=STERNE;
RX MEDLINE=99445483; PubMed=10515943;
RA Okinaka R.T., Cloud K., Hampton O., Hoffmaster A.R., Hill K.K.,
RA Kelm P., Koehler T.M., Lamke G., Kumano S., Mahillon J., Manter D.,
RA Martinez Y., Rieke D., Svensson R., Jackson P.J.;
RT "Sequence and organization of pX01, the large Bacillus anthracis
RT plasmid harboring the anthrax toxin genes.";
RL J. Bacteriol. 181:6509-6515(1999).
DR EMBL: AF065404; AAD32318.1; -.
KW Plasmid.
SQ SEQUENCE 564 AA; 66521 MW; D22C87DBA68DF021 CRC64;

Query Match 3.8%; Score 8; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 127 LYGSEKLT 134
    |||||
Db 329 LYGSEKLT 336

RESULT 13
Q922L9 ID Q922L9 PRELIMINARY; PRT; 964 AA.
AC Q922L9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO ATPase, CLASS II, TYPE 9A (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC006949; AAH06949.1; -.
FT NON_TER
SQ SEQUENCE 964 AA; 108661 MW; 377DEDA4D53BEC27 CRC64;

Query Match 3.8%; Score 8; DB 11; Length 964;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 PELYKDLL 208
    |||||
Db 824 PELYKDLL 831

RESULT 14
Q9KCV8 ID Q9KCV8 PRELIMINARY; PRT; 70 AA.
AC Q9KCV8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE BHI451 PROTEIN.
GN BHI451.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
```

RL Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001512; BAB05170.1; -.
KW Complete proteome.
SQ SEQUENCE 70 AA; 8093 MW; 53DCBAB438D7262A CRC64;
Query Match 3.3%; Score 7; DB 16; Length 70;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 GGFLGGL 14
| | | | | | |
DB 34 GGFLGGL 40
RESULT 15
Q9PE80
ID Q9PE80 PRELIMINARY; PRT; 101 AA.
AC Q9PE80;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ATP SYNTHASE C CHAIN (EC 3.6.1.34) (LIPID-BINDING PROTEIN) (SUBUNIT C).
DE C).
GN XFL148.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) /
CC HAS THREE MAIN SUBUNITS: A, B AND C (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
DR EMBL; AC003950; AAF83958.1; -.
DR HSSP; P00844; 1A91.
DR InterPro; IPR002379; ATPase_C.
DR InterPro; IPR000454; ATPase_C_eub.
DR Pfam; PF00137; ATP-synt.C; 1.
DR PRINTS; PR00124; ATPASEC.
DR PROSITE; PS00605; ATPase_C; 1.
KW CF(0); Complete proteome; Hydrogen ion transport; Lipid-binding;

KW Transmembrane.
SQ SEQUENCE 101 AA; 10255 MW; 7017ADA5B34C69F0 CRC64;
Query Match 3.3%; Score 7; DB 16; Length 101;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 ISVAVGL 107
| | | | | | |
DB 73 ISVAVGL 79
Search completed: October 21, 2002, 16:20:46
Job time : 65 secs